Dynamic Zero-Covid strategy curtails mutagenesis and emergence of new variants of the SARS-CoV-2

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Biological Sciences - Article

Keywords:

Posted Date: December 28th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-1195945/v1>

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Dynamic Zero-Covid strategy curtails mutagenesis and emergence of new variants of the SARS-CoV-2

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Abstract: Within the local outbreak period of SARS-CoV-2 Delta variant in Nanjing and Yangzhou, China, we analyzed the mutation process of the Delta variants in 520 cases, as well as the production, spread and elimination of new mutant strains under the non-pharmaceutical interventions (NPI) strategy. The investigation on distribution of COVID-19 cases and phylogenetic analysis of SARS-CoV-2 genome sequences attributed to tracking the transmission chains, transmission chains were terminated by the isolation of the COVID-19 patients and quarantine of close-contacts, suggesting the importance of NPI in prompting some mutations to disappear and stopping the transmission of new variants. Dynamic zero-Covid strategy has been implemented successfully to against the second-largest local epidemic caused by an imported COVID-19 case in China.

Main Text:

After almost two years, the coronavirus disease 2019 (COVID-19) pandemic continues to sweep across the globe. With the Delta variants dominating, the world is facing challenges to address the public health emergency. The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is prone to mutations like other RNA viruses. Genome sequencing of SARS-CoV-2 has shown a nucleotide substitution rate of $\sim 1 \times 10^{-3}$ per year¹. As of 3 December 2021, 3,245,521 variants have been identified from 5,893,087 SARS-CoV-2 sequences, where mutations have been mainly observed in the open reading frame (ORF) and spike (S) protein regions². Such changes in the genome may affect virus' properties such as pathogenicity, infectivity, and alter the effectiveness of vaccines, therapeutic medicines, and diagnostic tools³. The World Health Organization (WHO) has defined Variants of Concern (VOCs) and Variants of Interest (VOIs) based on their characteristics. A total of 5 VOCs (Alpha, Beta, Gamma, Delta and Omicron) and 2 VOIs (Lambda and Mu) have been described⁴. Currently, out of 839,119 genomes sequenced from the virus samples collected in the last 60 days, 837,253 (99.8%) belong to the Delta variant, 314 (<0.1%) to Gamma, 160 (<0.1%) to Alpha, 159 (<0.1%) to Omicron, 14 (<0.1%) to Beta, and <0.1% comprised other circulating variants (including VOIs Mu and Lambda). These statistics suggest that the Delta variants have become the dominant variants⁵. Concerningly, several studies have shown that the infectivity and viral loading caused by the Delta variants are increased when compared to wild type strains and other VOCs.⁶⁻⁸

The evolution of viruses is usually influenced by random mutations and the selective pressure exerted by drugs or immune responses elicited against the virus⁹. However, social control policies, such as measures of eradication and elimination, have profound influence on the course of epidemics by stopping or retarding the pace of viral natural evolution¹⁰. The zero-Covid strategy means eliminating all cases of SARS-CoV-2 from a country or region, which is different from eradication that means completely eradicating the source of the infectious disease. The eradication of infectious diseases has been achieved only once in history, with smallpox, a momentous achievement for global public health. Following intensive vaccination campaigns, in 1980, the 33rd World Health Assembly officially declared the world free from smallpox. Similarly, since 1988, significant effort has been put into the elimination of poliomyelitis viruses. Consequently, infections caused by the wild type (WT) poliovirus have decreased by over 99%. Of the 3 strains of WT poliovirus (type 1, type 2, and type 3), WT poliovirus type 2 was eradicated in 1999 and no cases of WT poliovirus type 3 have been reported since the last reported case in Nigeria in November 2012. This success has been largely accomplished by strengthening routine immunization, catch-up immunization and high-quality of AFP surveillance^{11,12}. Despite this success, complete eradication polio has been out of reach¹³⁻¹⁷. On 2021, WHO officially certified China as malaria-free after the country reported no indigenous cases of the disease for 4 consecutive years, following application of artemisinin, indoor residual spraying, roll-out insecticide-treated bed-nets, coupled with a 1:3:7 surveillance and response system¹⁸. Leprosy was eliminated through the non-pharmaceutical interventions (NPI) and pharmaceutical interventions (PI). Plague and Ebola have achieved elimination through international quarantine policies. Among the emerging infectious diseases, Nipah virus, Hendra virus and SARS virus have been basically eradicated through strict NPI measures. These experiences in eradication and elimination of diseases provide effective and referential ideas for the prevention and control of COVID-19.

NPI (to discover and isolate the source of infection) strategy was implemented during the epidemic prevention and control process in Wuhan, China. Remarkably, this strategy yielded

zero-covid cases in 76 days. In fact, while China has implemented the zero-Covid strategy successfully, attracting global attention, South Korea, New Zealand, Taiwan, Hong Kong, Macao, Australia along with other countries or regions are also working hard to implement the zero-Covid strategy. In the second-largest local epidemic caused by an imported COVID-19 case in Nanjing and Yangzhou, China, following the first-largest local epidemic in Wuhan, we systematically dissected the mutation process of the Delta variants in different individuals, as well as the production, spread and elimination of new mutant strains under the intervention of the NPI strategy.

1. Source and local spread of SARS-CoV-2 Variants

On July 10, 2021, a total of 301 passengers flying on the Boeing 777-300ER flight from Moscow, Russia arrived at Nanjing Lukou International Airport (NKG). When tested for COVID-19 at the time of entry using the SARS-CoV-2 RT-PCR test, five COVID-19 positive cases were detected amongst the arrivals. Subsequent genome analysis revealed that the passengers were infected with the Delta variants and one of the cases (Nanjing/Yu) carried very high loadings of the Delta variants ($C_t = 14.5$). Two COVID-19 cases were detected on the 5th and 7th day after arrival of the flight 777-300ER at NKG. However, the two cases are unlikely to be the source of infection that subsequently spread locally because they tested negative in the cabin. According to China's quarantine policy, all the arrivals are lodged in a hotel far from the NKG for quarantine and observed for 14 days immediately after disembarking from the plane. Therefore, the newly detected COVID-19 cases did not directly contact the infected COVID-19 cases among the arrivals. One hour after all the passengers and aircrew left the cabin and after prophylactic disinfection, 16 cleaning staff boarded the cabin to clean. Among them, 6 cases of COVID-19 were found during the weekly nucleic acid testing on July 20; five of them had a history of direct contact with the excreta or pollutants of the case-Nanjing/Yu, including two who cleaned the toilets which case Nanjing/Yu used, two cleaned the aisles where he walked through, and one cleaned up the garbage from Nanjing/Yu's seat. Although the cleaning staffs were wearing masks and gloves, the gloves did not cover the cuffs of the protective clothing. This may have caused their wrists to be exposed. Their hands were not disinfected during the process of cleaning, handling garbage and removing protective clothing after cleaning, and gloves were slipped off, which may have caused hand contamination. Through whole-genome sequencing analysis, it was found that they were infected with the Delta variants. The genomes of the virus isolated from the cleaning staff were highly homologous to those detected in case Nanjing/Yu, showing complete identity, including the spike H146Y mutation of SARS-CoV-2. No other COVID-19 cases from that flight had the spike H146Y mutation and showed low viral loadings. In addition, since July 1 to July 20, a total of six international flights arrived in Nanjing and some passengers have been found infected with SARS-CoV-2, but none of them carried the Delta variants. The outbreak among cleaning staff was not spatially related to the Guangdong and Yunnan outbreak, where local cases of Delta variants have been previously reported. Based on the epidemiological and genomic data, it can be inferred that the cleaning staff probably contracted COVID-19 through indirect contact with the case-Nanjing/Yu.

2. Indigenous spread of SARS-CoV-2

Nanjing is located on the East coast of China, with 9,314,685 permanent residents. From the onset of the outbreak of the epidemic at NKG on July 20th to September 9th, a total of 780 COVID-19 cases were reported in Nanjing and Yangzhou. In the Nanjing outbreak, the 10-day period between the cabin exposure and the discovery of the COVID-19 cases, the epidemic ran its natural course and was defined as “natural epidemic period, NE”. From July 21st to 26th, nucleic acid tests were carried out for close contacts and high-risk populations. Furthermore, hotel quarantine and treatment in designated hospitals for COVID-19 cases, closure and control of the communities where the cases were located were carried out. These measures could not yet achieve complete hotel quarantine for close contacts, so this 6-day period was termed as “incompletely intervened period, II”. Starting from July 27th and 9 days thereafter, nucleic acid tests for close contacts and high-risk populations were performed. Hotel quarantine and treatment in designated hospitals for cases, closure of the communities where the cases were located, and hotel quarantine of all close contacts were achieved. Therefore, this period was called “completely intervened period, CI”. The benefits of implementation of vigorous intervention started becoming visible after CI, with the number of COVID-19 cases dropping from over 10 COVID-19 cases per day to less, and the last case was detected on August 11. This phase was called as “epidemic regression period, ER”. During the NE, II, CI and ER period, the number of COVID-19 cases or nucleic acid positives found in Nanjing were 41, 109, 64 and 7, respectively (Fig. 1A).

Yangzhou is located about 100 kms to the Northeast of Nanjing. The epidemic in Yangzhou started from accidental exposure to a COVID-19 case of Nanjing on July 19. The patient travelled to Yangzhou on July 21. She was confirmed as COVID-19 positive by RT-PCR on July 27 in Yangzhou and intervention measures were put in place on July 28. The NE period was 9 days and a total of 48 COVID-19 cases occurred during this time. Hereafter, during the 10-day II period, 8-day CI period and 10-day ER period, 358, 141, and 12 COVID-19 cases were detected, respectively (Fig. 1B).

Phylogenetic analysis revealed that all the genomes of viruses isolated from COVID-19 patients of Nanjing and Yangzhou fell into one clade. The viruses from Yangzhou COVID-19 cases belonged to the branch of those from Nanjing COVID-19 cases, which was consistent with the fact that the COVID-19 local outbreak in Yangzhou originated from the old lady case (YZ001) who travelled from Nanjing to Yangzhou. None of the genomes from Yangzhou COVID-19 cases fell into the majority of genomes from Nanjing COVID-19 cases may due to the timely lockdown measure of Yangzhou. The genomes from Nanjing and Yangzhou COVID-19 cases were not clustered with those of early genomes of imported COVID-19 cases detected before July 10, 2021 in Mainland, China and the early Delta variants DL-ILBS-22053 isolated in New Delhi, India. (Fig. 1C).

3. Characteristics of mutations of the virus causing local epidemic

Compared with Wuhan-Hu-1 strain, the Delta variants isolated from case Nanjing/Yu and the early infected local cases in Nanjing had 35 mutations in the nucleotide sequence and three deletion sites (Extended data Table 1). The mutations seem to have changed many amino acids. Among them, there were four amino acid (aa) substitutions in the nucleocapsid protein (N), namely D63G, R203M, G215C and D377Y. There was one amino acid substitution, I82T, in the membrane protein (M). There were 16 amino acid substitutions in other ORF regions, including 11 substitutions in ORF1ab (K261N, A1306S, P2046L, P2287S, V2930L, T3255I,

T3646A, P4715L, G5063S, P5401L, A6319V), one substitution in ORF3a (S26L), three substitutions in ORF7a (P45L, V82A, T120I) and one substitution in ORF8 (ERF119-120DF) (Fig. 2A). G5063S (nucleotide G15451A) substitution in RdRp resulted in the mismatch of Charite primer, which may affect its detection efficiency because it mapped to the 3' primer region. Another R203M (nucleotide acid G28881T) substitution in N gene may have no influence on efficiency of the primer designed by China center for Disease Control and Prevention (China CDC) since its location maps to the first nucleotide of the 5' primer region (Fig. 2C). No amino acid substitution was observed in the envelope (E) protein, thus there is no effect on the diagnostic reagents targeting E protein. In addition to the impact of mutations on testing, previous studies have shown that mutations in the ORF1ab region may increase the viral load and cell mortality¹⁹, and probably be related to the decrease of lymphocytes (CD3⁺ T, CD4⁺ T, CD8⁺ T, CD19⁺ B cells and CD16⁺ CD56⁺ NK cells) and cytokine release (IL-6 and IL-8)²⁰. ORF3a mutations are probably likely to impact the viral life cycle, virulence, infectivity, ion channel formation, and virus release²¹. Furthermore, the deletion in ORF8 may reduce the virulence of SARS-CoV-2, resulting in harmless mild infections²². Moreover, SARS-CoV-2 hijacks the host ubiquitin system to enhance ORF7a's ability to antagonize IFN-I responses. Therefore, mutations in ORF7a would change the IFN-I signaling and affect viral mechanisms responsible for suppressing the immune response^{23,24}. Another study suggested that I82T substitution in M protein could affect the putative glucose transport transmembrane helices, leading to immune evasion²⁵.

The S protein of SARS-CoV-2 plays an important role in the infection process and therefore has received extensive attention. Among the 38 variations at different sites identified by comparing the genomes, eight amino acid substitution sites and one amino acid deletion are located in the S protein (Fig. 2B, Extended data Table 1). These include T19R, G142D, H146Y, L452R, T478K, D614G, P681R, D950N substitutions and the deletion of 156-157DEL. Within these, five amino acid substitutions (G142D, H146Y, D614G, L452R and T478K) and one amino acid deletion (157DEL) may be related to the reduced binding ability of existing neutralizing antibodies (Extended data Table 2)²⁶⁻³⁴. The P681R is located at the cleavage site of the furin protease, which makes the cleavage more efficient and the virus enters the host cell faster. It is also known to enhance the replication of virus, resulting in higher levels of viral loading and increased transmission³⁵⁻³⁷. It is worth mentioning that, the H146Y mutation in the S protein may further exacerbate the effects of vaccines and antibody-based interventions as predicted by modeling and results observed in the real world. According to the results of our previously published studies, the H146 site of NTD in SARS-CoV-2 S protein is an important neutralization site, which has strong binding activity with neutralizing antibodies like FC05²⁸. The neutralizing antibody (4A8) reported by Wei Chen et. al. also showed similar properties²⁹. According to the GISAID database, Delta variants containing the S protein H146Y mutation were reported from 8 countries, including Russia, before July 10th³⁸.

4. Mutations of SARS-CoV-2 under dynamic zero-Covid strategy

Several transmission chains were formed in the local epidemic caused by the Delta variants where a wide range of single nucleotide variations (SNV) were observed. These included the 35 basic mutation (nucleotide mutation, including H146Y mutation), 35 basic & n iSNV (rare) mutation (n≥1), 35 basic+C346T mutation, 35 basic+ C346T & n iSNV (rare) mutation (n≥1), 35 basic+T2803C mutation, 35 basic+ T2803C & n iSNV (rare) mutation (n≥1), 35

basic+T2803C+T7513C mutation and 35 basic+T2803C+T7513C & n iSNV (rare) mutation ($n \geq 1$), respectively. (Fig. 3)

Among the 221 COVID-19 cases in Nanjing, whole-genomic sequences of 167 cases were successfully compiled. Sequence analysis revealed that a total of 48 SNV combinations were formed, mainly including C346T or T2803C homozygous mutations, and other rare homozygous mutations of the C346T or T2803C type (Fig. 3A, Extended data Table 3 and Table 5). The number of SNV combinations formed in NE, II, CI, and ER periods were 16, 17, 13, and 2, respectively (Fig. 3C). Among these 48 SNV combinations, 39 were terminated in complete hotel quarantine, and 9 were spontaneously terminated. The spontaneously terminated cases had the opportunity to infect others. Thus, about 81.25% (39/48) of mutations were terminated by hotel quarantine measures. Specifically, 3, 17, 15 and 4 SNV combinations were terminated with NPIs in NE, II, CI, and ER periods, while 2, 5 and 2 SNV combinations were self-terminated in NE, II and CI periods, respectively. In addition, several SNV combinations emerged in single cases. As shown in Fig.3C, 5, 14, 8 and 1 SNV combinations terminated in NE, II, CI, and ER periods, of which 3, 8, 7 and 1 were terminated by hotel quarantine measures, and others were self-terminated in the four periods, respectively.

Among the 559 COVID-19 cases in Yangzhou, 353 whole-genome sequences were obtained and 89 SNV combinations were identified (Extended data Table 4 and Table 6). Based on epidemiological evidence, the unique original case in Yangzhou was an old lady YZ001, with T2803C mutation add to the 38 basic nucleotide mutations in Nanjing, secondary transmission from NJ047, who was firstly observed with the T2803C substitution during the early II' period in Nanjing, so all cases had 36 basic mutations in Yangzhou. Sequence analysis revealed that T7513C homozygous mutations were added, and other rare homozygous mutations with T7513C or T2803C type (Fig. 3B). The number of SNV combinations formed in NE, II, CI and ER periods were 15, 44, 28, and 2, respectively. Of the 89 SNV combinations, 53 were terminated in complete hotel quarantine, and 36 were self-terminated. The self-terminated cases had the chance to infect others. The mutations terminated due to hotel quarantine accounted for 59.55% (53/89) (Fig. 3D) of the total cases, which was lower than that of Nanjing. This discrepancy could be attributed to the longer II period. Specifically, 2, 21 and 30 SNV combinations were terminated with NPIs in NE, II and CI periods, while 6, 15, 12 and 3 were self-terminated in NE, II, CI and ER periods, respectively. Several SNV combinations were also found in single cases in Yangzhou (Fig.3D), 7, 28, 22 and 2 SNV combinations terminated in NE, II, CI, and ER periods, of which 2, 16, 13 and 0 were terminated by hotel quarantine measures, and others were self-terminated in the four periods, respectively.

In this epidemic, the elimination of the Delta variants included two aspects. On one hand, the self-elimination of the Delta variants could terminate the transmission chain in the absence of NPI, the percentage of mutants eliminated in self-termination accounted for 32.85% of the total SNV combinations. On the other hand, the number of the SNV combinations decreased gradually from II to ER periods, and eventually the transmission chains were fully terminated, suggesting that hotel quarantine could effectively prompt some mutations to disappear and was important to stop the SNV combination of Delta variants in local epidemic.

Respiratory samples were collected from three COVID-19 cases at different time points to analyze the dynamics of the allele frequency in intra-host single nucleotide variations (iSNVs). Changes in the profiles of alternative allele frequencies (AAFs) were noted for samples collected at three different dates. Four iSNVs including T12175A, T16392C, G24410A (YZ409), and G28916T (YZ404) showed an increase in frequency and remained stable during

second and third sampling. Two iSNVs including C23604G and C27527T (YZ409 and YZ404) showed high AAFs during first two sampling dates which decreased in third sampling date. Three iSNVs including G21987A, C27527T and G28916T (YZ018) displayed decreased AAFs during the second sampling date while having high AAFs in first and third sampling dates. Noteworthily, we observed some minor AAFs such as C7764T spontaneously disappear within the host, while T7513C (YZ018) continuously evolve and become homozygous at third sampling date (Fig. S1). T7513C substitution was a common SNP that emerged in more than 89 cases of Yangzhou epidemic. Quarantine of COVID-19 patients with YZ018 profile further confirmed zero-Covid strategy would help to stop the spread of the mutation and terminate the further evolution of the virus.

5. Impact of the mutations on the epidemiology of COVID-19

We analyzed the whole-genome sequence data obtained from 520 cases, which included 371 non-terminated cases and 149 terminated cases by multivariate logistic regression model. Only onset period of cases in the epidemic, COVID-19 vaccination state (Vaccinated $\geq$ 30days) and clinical symptoms (Severe+Critical) were associated with termination of SNV combinations, while age, sex, Ct Value (viral loading), clustering and termination codon were not associated with termination of SNV combinations (Extended data Table 7). The termination rates of the last cases were higher in II and CI periods compared to NE and ER periods. Vaccinated cases ($\geq$ 30days) were 2.33 times more likely to have their SNV combinations terminated than those who were not vaccinated, which could be related to the presence and known consequences of E484K/Q substitution, in spite of H146Y substitution in S protein region in the local Delta variants³⁶.

In the local epidemic, based on whole-genome sequence analysis, G28209T located in ORF8b region results in a stop codon, terminating the synthesis of the peptide chain. The G28209T mutation was noted in several transmission chains among 8 cases in Nanjing, including 2 cases in 35 basic + C346T & 1 iSNV mutation chain and 6 cases in 35 basic + C346T & niSNV (rare) mutation chain. Four of them were the last COVID-19 cases, of which three were terminated by NPI and only one was stopped by self-termination, indicating the important role of NPI in stopping the transmission of variants with G28209T mutation. In previous studies, ORF8b protein of SARS-CoV-2 could trigger the activation of the NLRP3 inflammasome in macrophages in vitro and mediate release of interleukin-1 family cytokines. Therefore, an intense inflammasome formation characterizes the lungs of patients with fatal COVID-19 disease due to pneumonia and acute respiratory distress syndrome (ARDS)³⁹. Published studies have indicated that the deletion of 382 nucleotides in the ORF8 region of the SARS-CoV-2 variants could result in less systemic release of pro-inflammatory cytokines and milder infections, while the patient's symptoms last longer²². Another study found a mutation (Q27stop) that truncated the ORF8 region in the VOC-202012/01 variant, the deletion in ORF8 changed the clinical onset of the disease, which may mediate immune escape and affect the transmission of SARS-CoV-2 variants⁴⁰.

Throughout this local epidemic, 81 amino acid mutations were found in different regions of SARS-CoV-2 among all cases, including 1, 3, 5, 11, 53, 2, 3 and 1 in E, M, N, S, ORF1ab,

ORF3a, ORF7a and ORF10 domains respectively. Another 2 additional mutations (nucleotide A27010C and A5289T) have not been defined in previous sequences. Eleven novel mutations in the S protein like L5F, P384S, N542K, D574Y, A647S, H655Y, G769V, V951L, Q1005H, T1117I, and Q1208H are worthy of attention. Among these, L5F has been found in several variants around the world, especially in B.1.526, which may be related to the increased transmissibility of the variant strain. This probably resulted in the second wave of COVID-19 cases to extend its duration in New York in early 2021 ⁴¹. H655Y mutation emerging in B.1.1.529 variants and P.1 variants has been proven to evade neutralization by human monoclonal antibodies, and can spread rapidly in cats and persists at intermediate frequencies ^{4,42}. In relation to the local epidemic, H655Y mutation was found among 6 sporadic cases in Yangzhou during the II and CI periods (from Aug 2nd-10th) and none subsequently cases, suggesting that the transmission of variants with this mutation may be terminated by the NPI measures. The G769V mutation was found in the R.1 lineage of SARS-CoV-2 in Japan. This mutation is not considered to be related to immune escape variants like the simultaneous E484K and W152L mutations, and its role needs to be further investigated ⁴³. T1117I mutation in the spike was found during the pandemic wave beginning in May 2020 in Costa Rica, whose frequency reached 29.2% in full genome analyses. Structural modeling of the T1117I mutation suggests a potential effect on the viral oligomerization needed for cell infection, but no differences with other genomes on transmissibility, severity nor vaccine effectiveness are predicted for this mutation ⁴⁴. In terms of the other 7 mutations, which were firstly identified and their information uploaded in GISAID database, the information of mutated locus and the corresponding biological changes in the function have not been reported. As can be analyzed from the chemical structure, the Q1005H and Q1208H substitution may abrogate intra-protomer hydrogen bond (H-bond) between the T716 side-chain and main-chain carbonyls of Q1005 and Q1208, but could form a symmetric histidine triad near the base of the spike. In addition, water-mediated interactions could promote the formation of hydrogen bonding between the histidines ⁴⁵. In terms of A647S mutation, after the hydrophobic and non-polar alanine converted to hydrophilic and polar serine, the hydroxyl group contained in serine may bind to the oligosaccharide chain of T645 and would lead to the changes of spatial structure between antigens and cells. Furthermore, the D574Y mutation would also be affected by glycan chains of T572 and T573 and may mediate immune escape, although its specific effects have not been confirmed in predicted models and the real world.

Discussion

At present, the Delta variants have become dominant worldwide. Countries that have significantly reduced the COVID-19 cases through vaccination have once again experienced an increase in cases; the rate of increase in cases being much faster than before. Immune escape of variants, leading to the immune protection obtained from vaccines and natural infections becoming ineffective, remains the biggest nightmare of mankind. From this perspective, the highly infectious Delta variants squeezing out the Beta variants with strong immune escape activity seem to help humans escape a catastrophe. Lessons learned from the successful control of local epidemics in Nanjing and Yangzhou, suggesting a key role for the analysis of mutations for case tracing and epidemic control, which prevented the formation of a dominant mutation due to the success of NPI measures that cleared COVID-19 cases. Many global teams are working to prevent and control the continuous variation observed in viruses. In fact, some of the models established based on bioinformatics and structural prediction could predict the

location and nature of possible mutations in future, and the prediction results were confirmed later in the strains that emerged later in the course of the epidemic⁴⁶⁻⁴⁸. Finally, admittedly, there are some limitations in this research. The impact of the amino acid mutations on the spike conformation have not been verified by cryo- electron microscopy (EM) in the current study, and the impact of the mutations on glycosylation remains to be analyzed. However, as these mutations have not been discovered in previous studies and the variants had been wiped out, and the local epidemic is not significantly different from previous reports. In addition, glycosylation analysis requires a large number of viruses and individual differences in glycosylation between hosts are the limitations of the method itself. Therefore, the mechanism of these mutation sites is planned to be investigated in our future researches and will be shown in another complete report.

As long as the virus continues to spread, it will replicate and produce new mutation sites. Only extensive vaccination and strict public health management are the best means to reduce risks of contracting COVID-19. The local mutation patterns discovered in Nanjing and Yangzhou, as well as the effective preventive and control measures adopted, have greatly reduced the development of global mutations and made outstanding contributions to the development of global public health and the reduction of disease burden. It would also provide reference methods and ideas for the prevention and control of new outbreaks in the future.

Online content

Any methods, statements of data and code availability, acknowledgements, details of author contributions, competing interests and References, and extended data are available at supplementary materials.

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Fig.1. Distribution of COVID-19 cases and phylogenetic analysis of SARS-CoV-2 genome sequences in Nanjing (A) and Yangzhou (B), 2021. (A, B) Time series and laboratory-confirmed COVID-19 cases in Nanjing and Yangzhou, respectively. Daily number of cases in natural epidemic period (NE), incompletely intervened period (II), completely intervened period (CI), and epidemic regression period (ER) are shown in blue, yellow, red, and green,

respectively. (C) The time resolved phylogenetic tree was constructed with the Nextstrain pipeline by including early imported COVID-19 cases detected before July 10, 2021 in Jiangsu province, delta variants of the local cases in Guangdong and Yunnan province detected in the period between March to July, 2021, and the early Delta variants DL-ILBS-22053 isolated in New Delhi, India. The sequences from the local COVID-19 cases of Nanjing (orange) and Yangzhou (blue) are highlighted with a red box and shown in panel C (inset).

Fig. 2. Genomic variance of the case Nanjing/Yu and its impact on diagnosis. (A) The position of 38 variations in the genome. (B) Variations in the spike mapped to the spike trimer. Structure made by PyMOL using PDBID 7A94. (C) Mutations in the real time PCR detection primer region. G15451A mutation in RdRp resulted in the mismatch of Charite primer which may affect its

detection efficiency because it mapped to the 3' primer region. Another G28881T mutation in N gene may have no effect on the efficiency of China CDC primer since it maps to the first nucleotide of the 5' primer region. Fig. 2B and Fig. 2C were made by Biorender (<https://biorender.com/>).

Fig. 3. SNV combinations under zero-Covid strategy. (A) The distribution of different SNV combinations of Nanjing COVID-19 cases in different epidemic periods. The scatter indicated the different SNV combinations among the cases, and the connected line indicates that a certain SNV combination of mutations appears in related cases. **(B)** The distribution of different SNV combinations of Yangzhou COVID-19 cases in different epidemic periods. The scatter indicated the different SNV combinations among the cases, and the connected line indicates that a certain combination of mutations appears in related cases. **(C)** The number of SNV combinations formed in the 4 epidemic periods in Nanjing and that only appeared in a single case, the self-

terminated number of transmission chain, the number of terminated transmission due to NPI measures. **(D)** The number of SNV combinations formed in the 4 epidemic periods in Yangzhou and that only appeared in a single case, the self-terminated number of transmission chain, the number of terminated transmission due to NPI measures.

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Extended data (Fig. 1, Tables 1 to 10)

Extended data Figure 1 | Temporal dynamics of intra-host populations in patients YZ404, YZ409 and YZ018.

Extended data Table 1 | Mutation sites of Delta variants from case Nanjing/Yu.

Extended data Table 2 | Distribution and observed effect of mutations and deletions in Spike protein.

Extended data Table 3 | Mutation Combinations of Nanjing.

Extended data Table 4 | Mutation Combinations of Yangzhou.

Extended data Table 5 | Summary table of Nanjing-Major combinations of mutations.

Extended data Table 6 | Summary table of Yangzhou-Major combinations of mutations.

Extended data Table 7 | SNV combinations can be terminated by NPI and vaccine.

Extended data Table 8 | Demographic characteristics of COVID-19 cases in Nanjing and Yangzhou.

Extended data Table 9 | Key reagents.

Extended data Table 10 | Sample and sequencing information. Related to Figure 1C.

Supplementary Materials for

Dynamic Zero-Covid strategy curtails mutagenesis and emergence of new variants of the SARS-CoV-2

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Materials and Methods

Ethics

Ethical approval for this study was approved by ethics committee of the Jiangsu Provincial Center for Disease Control and Prevention. Written informed consent was waived in light of the urgent need to collect data.

Epidemiological investigation of populations

COVID-19 cases in Nanjing and Yangzhou were included in this study, whose demographic characteristics were described in Extended data Table 8. Similar distribution of sex, CT values and clinical type were observed in Nanjing and Yangzhou, as well as age, except for the subgroup of '[40-50]' and '≥60'. Cases in Nanjing and Yangzhou were comparable regarding cluster distribution; 450/559 (80.50%) cases were classified into clustered group in Yangzhou, while in Nanjing, this proportion was 32/221 (14.50%). The differences are probably caused by differences in daily activities of the cases in Yangzhou. In addition, a significantly higher proportion of non-vaccination subgroup existed in Yangzhou when compared to Nanjing, may be for the reason that most of the cases in Yangzhou were the elderly or children who have not been immunized.

Verification of diagnosis and epidemiological investigation were conducted for each newly detected COVID-19 nucleic acid positive case. The verification of diagnosis included rechecking the first positive specimen and re-collecting the patient's nasal/pharyngeal swab specimens within 24 hours for nucleic acid testing. Patients with positive nucleic acid test at least twice were included in this study.

Epidemiological investigation includes the following four parts. (1) Investigation of clinical manifestations (whether there are symptoms, first symptoms and onset time) and the sampling time of the first positive nucleic acid test of COVID-19; (2) Activities of the infected person within 14 days before the onset time or the sampling time of first positive test, focus on investigating whether the contacts have been identified as infected, and investigating the date, duration, frequency, and protection of contact methods with the infected persons. In addition, exposure to objects or environment contaminated by infected persons, including exposure to foreign aircraft, exposure to environments in which known cases have been active or the contact with contaminated items (duration, frequency, exposure methods, protection conditions, and environmental characteristics). These activities help to determine the source of infection, assist in inferring the possible time of infection, and thus analyze the transmission relationship. (3) Close contacts, those who were in contact before symptom onset or 4 days before the first positive test, or those who were exposed to the same small confined space together with them, were defined as close contacts. (4) Sub-close contacts, a person who has been in contact with a close contact from contacting with an infected person to hotel quarantine was defined as a sub-close contact.

Through epidemiological investigation, clarify the transmission chain of the cluster epidemic and determine whether each infected person has continued transmission. If it is judged that there is no further spreader, it is determined as the last case of a transmission chain, and the infection period can be inferred based on the detection time or onset time of the last infected person. If a case has been quarantined before the infectious period, the termination of the variant transmission is considered to be due to non-drug intervention (NPI) measures. If a case has not been fully controlled during the infectious period but no transmission occurs, the termination of the variant transmission is considered to be due to self-termination of the virus.

Non-pharmaceutical interventions (NPI)

(1) Management of COVID-19 cases. Confirmed cases were transferred to designated infectious disease institutions within 2 hours for treatment, observation or quarantine, until they meet the discharge standards of the “Diagnosis and Treatment Protocol for COVID-19”.

(2) Management of close contacts. Close contacts were transferred to the hotel quarantine within 12 hours after discovery, and take a single hotel room to quarantine until 14 days after contact with an infected person (people with difficulties in living on their own are allowed to be isolated at home or accompanied by someone), and respiratory samples were collected on the 1, 4, 7, 14 days of the quarantine period for testing nucleic acid of SARS-CoV-2. Two nasopharyngeal swabs were collected on the 14th day, and were tested by two reagents separately. Those who tested negative during the quarantine period were released and be monitored at home for 7 days after release. They were not allowed to participate in gathering activities during the period and were suggested to take nucleic acid tests on the 2nd day and 7th day respectively, then the control would be lifted after all negative results of nucleic acid tests.

(3) Management of sub-close contacts. They were transferred to a centralized quarantine place within 12 hours and quarantine in a single room of a hotel for 7 days. If those close contacts they contact were tested negative within 4 days before quarantine, these sub-close contacts would be released after testing negative on the 1st, 4th or 7th day. If those close contacts were tested positive, these sub-close contacts will be determined as close contacts for further control.

(4) Closed management of the community. Communities with community transmission or communities with more than 5 cases were closed for management. People in the communities were not allowed to leave their homes, and supplies were uniformly distributed after secondary protection by community management personnel. The nucleic acid tests were performed among persons in the communities on the 1st, 4th, 7th and 14th day of management. The control would be lifted until no new cases appear in the community over 14 days after the cases left the community.

(5) Containment management of the community. The communities where cases have occurred, then people in the community are not allowed to leave the community, while one person in each family is allowed to purchase daily necessities in or near the community. The control would be lifted until no new case appear in the community over 14 days after the cases left the community and all persons in the community are negative by nucleic acid screening within 14 days.

(6) Other social management. Districts and counties affected by the epidemic were temporarily closed all business places, such as chess and card rooms, activity rooms, cinemas, KTV, bars, amusement parks, museums and other leisure places that are not necessary for daily life, while other places that are necessary for daily life will take control measures such as limiting traffic, shortening and adjusting business hours.

(7) Nucleic acid screening: nucleic acid screening was carried out for all members of communities involved in the occurrence and activities of cases, so as to determine the spread of infection and further adjust the scope of control. During the epidemic period, all members were screened for nucleic acid every 3 to 5 days. Whether to carry out the next round of testing and the time and scope of testing was determined according to the test results and the development trend of the epidemic. If there were newly infected persons who were not under control, screening would continue to be carried out in their activity areas. If all new cases occur in the controlled population, screening would not be carried out.

Nucleic Acid Extraction and Viral RNA Detection of SARS-CoV-2

Upper respiratory specimens (nasopharyngeal and oropharyngeal swabs) were collected from all suspected cases. Total RNA was extracted from 200 µL of the specimens using a magnetic

bead-based viral RNA nucleic acid extraction system (TianLong Technologies, Xian, China). Then, qRT-PCR was performed using a 2019-nCoV RNA detection kit (BioGerm Medical Technologies, Shanghai, China). Conditions for the reaction were as follows: 50°C for 10 min and 95°C for 5 min, followed by 45 cycles of amplification at 95°C for 10 s and 55°C for 40 s. Amplification and detection were performed with the QuantStudio7 Pro Real-Time PCR Systems (Thermo Fisher Scientific, MA, USA) according to the manufacturer's instructions. Data were analyzed using the software supplied by the manufacturer. Sample was positive if the cycling threshold (CT) values of qRT-PCR for the ORF1ab and the N genes were less than 37. Sample was deemed negative if no CT value, or CT value of greater than 40, or unrepeatability CT value in the range of 37-40 were obtained. Tests meeting both ORF1ab and NP gene positivity criterion simultaneously were considered positive.

Virus amplification and sequencing

For samples with qRT-PCR Ct value ≤ 34 , whole genome was amplified using target specific multiplex PCR amplification kit (Beijing MicroFuture, BAIYITECH, MGI, China, and Thermo Fisher, USA) according to manufacturer's instructions. PCR products were purified using AmpureXP beads (Beckman Coulter, USA) and quantified using fluorimetry with the Qubit dsDNA High Sensitivity assay on the Qubit 2.0 instrument (Life Technologies, USA) (Extended data Table 9). After DNA sequencing Library was constructed, sequencing of libraries was conducted on the Illumina (Miseq, MiniSeq, NextSeq2000, and iSeq100), BGI (MGISEQ-2000), Thermo Fisher (S5XL and GenexusTM) sequencing platform (Extended data Table 10). The original sequencing data were firstly cut off the amplification primer sequences. Then, reads were trimmed to remove low-quality bases and assembled into a genome consensus sequences using Wuhan-Hu-1 (GenBank:MN908947.3) as reference in the CLC Genomics Workbench (Version 21.0) software. For variant detection, base quality larger than 20, the minimum coverage 100, count 10 and frequency 10% were set. Variants were called also using Wuhan-Hu-1 as reference.

Phylogenetic analysis

A total of 537 (167 cases from Nanjing outbreak, 353 cases from Yangzhou outbreak, seven imported cases related to Delta variants, four cases from Guangdong outbreak and four cases from the Yunnan outbreak of Delta variants, Wuhan-Hu-1, and the early Delta variants DL-ILBS-22053 listed in Extended data Table 10) near-complete and complete genomes were aligned using MAFFT v7.487.¹ The resulting dataset were used to estimate maximum likelihood (ML) phylogeny using IQTree V.2.² The time resolved phylogenetic tree was constructed with the Nextstrain pipeline³.

Statistical analyses

In this real-world study, we included all 520 cases from which genome-wide data were obtained during an outbreak in Nanjing and Yangzhou from July 13 to August 25, 2021. Demographic and laboratory data were obtained from the stream database, and the combined mutation data for each case were summarized and compared. Descriptive analyses of demographic data are presented as mean when continuous and as frequency and ratio (%) when categorical. Univariate and multivariate logistic regression methods were used to investigate the factors influencing whether the SNV combinations could be terminated. Six variables were selected for multivariate analysis based on preliminary statistical findings and clinical limitations. Statistical

analyses were done using IBM SPSS18.0 and R (Version 9.3). A two-sided α of less than 0.05 was considered statistically significant.

Statements of data and code availability: All sequencing reads after primer trimming have been submitted to the National Genomics Data Center (<https://ngdc.cnbc.ac.cn/>) with submission number CRA005588. The generated consensus sequences were submitted with accession number GWHBGC01000000-GWHBGWF01000000. All other data are available in the manuscript or the supplementary materials, and the results supporting the findings in this study are available upon request from the corresponding authors.

Acknowledgements: We thank Jingyu Lou, Yue Ding and Jinmei Qian for their support with the sequencing and quality control, Nan Zhou, Xin Zhou, Jie Ding, Qin Xu, Tao Ma, Xiang Huo, Yue Dai, Yang Zhou, Lingen Shi, Na Sun, Wei Wang, Chuanwu Sun, Yalong Wang, Yanmin Zhou, Liling Chen, Zhiquan Wang, Yanmin Mao, Zheng Zhang, Hao Xue, Cuiying Chen and Lei Wang for technical assistance with epidemiological investigation. We thank the Jiangsu Provincial Key Research and Development Program BE2021738 and National science foundation of Jiangsu province (BK2021373, BE2019761).

Details of author contributions: FC.Z., and LB.C., conceptualized and provided funding for this study, LB.C., LG.Z., YY.G., SJ. W., X.H., XS.G., X.Q., JG.F., ZF.L., H.F., HY. Y., F.D., KC.Z., XJ.Z., J.L., and HD.L., did the methodology part, J.Z., HF.F., YX.Y., J.Z., JL.H., JJ.L., J.A., GD.K., Y.S., GJ.J., FR.W., Z.Z., M.H., SN.D., Y.W., YU.D., HM.Y., CH.Y., LY.W., YD.J., JF.W., JX.L., CJ.B., and M.W., investigated the data, M.W., FC.Z., and LB.C administrated this project, LB.C., X.H., and XS.G. wrote the original draft, FC.Z., and LB.C review and edit this paper. LB.C., LG.Z., J.Z., HF.F., YX.Y., J.Z., YY.G., and SJ.W. contributed equally to this study.

Competing interests: All authors declare no competing interests.

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Extended data Figure 1 | Temporal dynamics of intra-host populations in patients YZ404, YZ409 and YZ018. Alternative allele frequencies (AAFs) among sampling dates in patients YZ404 (A), YZ409 (B) and YZ018 (C). Days post the first symptom date are shown in the abscissa. Colors represent different iSNVs.

Extended data Table 1| Mutation sites of Delta variants from case Nanjing/Yu.

Mutation site	Protein (number of substitutions)	INFO
2019-nCoV_210	ORF1ab (16)	VEP=upstream gene variant, DISTANCE=56, QHD43415.1,gene-orf1ab
2019-nCoV_241		VEP=upstream gene variant, DISTANCE=25, QHD43415.1,gene-orf1ab
2019-nCoV_3037		VEP=synonymous_variant,QHD43415.1:p.924F,gene-orf1ab:c.2772ttC>ttT
2019-nCoV_8986		VEP=synonymous_variant,QHD43415.1:p.2907D,gene-orf1ab:c.8721gaC>gaT
2019-nCoV_11332		VEP=synonymous_variant,QHD43415.1:p.3689V,gene-orf1ab:c.11067gtA>gtG
2019-nCoV_1048		VEP=missense_variant,QHD43415.1:p.261K>N,gene-orf1ab:c.783aaG>aaT
2019-nCoV_4181		VEP=missense_variant,QHD43415.1:p.1306A>S,gene-orf1ab:c.3916Gct>Tct
2019-nCoV_6402		VEP=missense_variant,QHD43415.1:p.2046P>L,gene-orf1ab:c.6137cCa>cTa
2019-nCoV_7124		VEP=missense_variant,QHD43415.1:p.2287P>S,gene-orf1ab:c.6859Cct>Tct
2019-nCoV_9053		VEP=missense_variant,QHD43415.1:p.2930V>L,gene-orf1ab:c.8788Gta>Tta
2019-nCoV_10029		VEP=missense_variant,QHD43415.1:p.3255T>I,gene-orf1ab:c.9764aCc>aTc
2019-nCoV_11201		VEP=missense_variant,QHD43415.1:p.3646T>A,gene-orf1ab:c.10936Act>Gct
2019-nCoV_14408		VEP=missense_variant,QHD43415.1:p.4715P>L,gene-orf1ab:c.14144cCt>cTt
2019-nCoV_15451		VEP=missense_variant,QHD43415.1:p.5063G>S,gene-orf1ab:c.15187Ggt>Agt
2019-nCoV_16466		VEP=missense_variant,QHD43415.1:p.5401P>L,gene-orf1ab:c.16202cCa>cTa
2019-nCoV_19220		VEP=missense_variant,QHD43415.1:p.6319A>V,gene-orf1ab:c.18956gCt>gTt
2019-nCoV_21618	Spike (8)	VEP=missense_variant,QHD43416.1:p.19T>R,gene-S:c.56aCa>aGa
2019-nCoV_21987		VEP=missense_variant,QHD43416.1:p.142G>D,gene-S:c.425gGt>gAt
2019-nCoV_21998		VEP=missense_variant,QHD43416.1:p.146H>Y,gene-S:c.436Cac>Tac
2019-nCoV_22917		VEP=missense_variant,QHD43416.1:p.452L>R,gene-S:c.1355cTg>cGg
2019-nCoV_22995		VEP=missense_variant,QHD43416.1:p.478T>K,gene-S:c.1433aCa>aAa
2019-nCoV_23403		VEP=missense_variant,QHD43416.1:p.614D>G,gene-S:c.1841gAt>gGt
2019-nCoV_23604		VEP=missense_variant,QHD43416.1:p.681P>R,gene-S:c.2042cCt>cGt

2019-nCoV_24410		VEP=missense_variant,QHD43416.1:p.950D>N,gene-S:c.2848Gat>Aat
2019-nCoV_25469	ORF3a (1)	VEP=missense_variant,QHD43417.1:p.26S>L,gene-ORF3a:c.77tCa>tTa
2019-nCoV_26767	Membrane (1)	VEP=missense_variant,QHD43419.1:p.82I>T,gene-M:c.245aTc>aCc
2019-nCoV_27527	ORF7a (3)	VEP=missense_variant,QHD43421.1:p.45P>L,gene-ORF7a:c.134cCa>cTa
2019-nCoV_27638		VEP=missense_variant,QHD43421.1:p.82V>A,gene-ORF7a:c.245gTt>gCt
2019-nCoV_27752		VEP=missense_variant,QHD43421.1:p.120T>I,gene-ORF7a:c.359aCa>aTa
2019-nCoV_27874	ORF8 (1)	VEP=upstream gene variant, DISTANCE=20,QHD43422.1,gene-ORF8
2019-nCoV_28461	Nucleocapsid (4)	VEP=missense_variant,QHD43423.2:p.63D>G,gene-N:c.188gAc>gGc
2019-nCoV_28881		VEP=missense_variant,QHD43423.2:p.203R>M,gene-N:c.608aGg>aTg
2019-nCoV_28916		VEP=missense_variant,QHD43423.2:p.215G>C,gene-N:c.643Ggt>Tgt
2019-nCoV_29402		VEP=missense_variant,QHD43423.2:p.377D>Y,gene-N:c.1129Gat>Tat
2019-nCoV_29742	ORF10 (1)	VEP=downstream gene variant, DISTANCE=68,QHI42199.1,gene-ORF10

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239 **Extended data Table 2 | Distribution and observed effect of mutations and deletions in Spike protein.**

Mutation site	Effects	Ref.
T19R	—	—
G142D	G142D reducing neutralization by the BNT162b2 immune sera ⁴ and the mAb 2489 ⁵ .	[4] Nature. 2021;10.1038/s41586-021-03693-y. [5] Nat Med. 2021;27(4):717-726.
H146Y	H146Y reducing neutralization by the mAb FC05 ⁶ and 4A8 ⁷ .	[6] National Science Review. 2021; nwab053. [7] Science. 2020; 369(6504):650-655.
△E156	—	—
△F157	F157A reducing neutralization by the mAb 2489 ⁸ .	[8] Cell. 2021;184(9):2316-2331.
R158G	—	—
L452R	L452R reducing neutralization by the mAb FC08 ⁶ , COV2-2096 ⁹ , SARS2-01, SARS2-02 and SARS2-32 ¹⁰ , C643 and C628 ¹¹ , and convalescent plasma ¹² .	[8] National Science Review. 2021; nwab053. [9] Cell Host Microbe. 2021;29(1):44-57. [10] Cell Host Microbe. 2021;29(3):477-488. [11] Nature. 2021;592(7855):616-622. [12] Cell. 2020;182(5):1284-1294.
T478K	T478I reducing neutralization by the mAb SARS2-16, SARS2-19 and and convalescent plasma (13 and 35#). ¹⁰	[10] Cell Host Microbe. 2021;29(3):477-488.
D614G	D614G could enhance virus infectivity and thermal stability, D614G does not significantly affect the effectiveness of existing vaccines, but may weaken the neutralizing activity of certain specific antibodies. ¹³	[13] Sci China Life Sci. 2021;64(7):1062-1067.
P681R	P681R may have increased replication, which leads to higher viral loads and increased transmission. ¹⁴	[14] N Engl J Med. 2021; 385(7): 585-594.
D950N	—	—

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Extended data Table 3 | Mutation Combinations of Nanjing.

Combination of Mutation	Date of onset of first case	Date of onset of last case	Total number of cases (controlled/un-controlled)	Number of cases in control period	Number of cases in uncontrolled period
Basic Mutation (same with Nanjing/Yu)	2021/7/13	2021/7/31	51(28/23)	26	25
C8819T	2021/7/26	2021/7/26	1(0/1)	0	1
T2803C	2021/7/29	2021/7/31	19(14/5)	11	8
T2803CC15738T	2021/7/28	2021/7/28	1(1/0)	1	0
T2803CG16968T	2021/7/28	2021/8/2	2(1/1)	2	0
A27133T	2021/7/31	2021/7/31	1(1/0)	1	0
C1060TC14573TC14576GT14562C	2021/7/26	2021/7/26	1(1/0)	0	1
C1385T	2021/7/22	2021/7/22	1(1/0)	0	1
C16289T	2021/7/31	2021/7/31	1(1/0)	1	0
C16289TA2467G	2021/8/1	2021/8/4	2(2/0)	2	0
C17402T	2021/8/2	2021/8/2	1(1/0)	1	0
C18828T	2021/7/20	2021/7/26	6(5/1)	0	6
C22642T	2021/7/22	2021/7/24	2(1/1)	0	2
C22642TC9165T	2021/7/30	2021/7/30	1(1/0)	1	0
C346T	2021/7/13	2021/7/27	14(8/6)	2	12
C346TA6411G	2021/7/20	2021/7/23	2(2/0)	0	2
C346TC1060T	2021/7/20	2021/7/25	9(7/2)	0	9
C346TC1060TC14708T	2021/7/25	2021/7/25	1(1/0)	0	1
C346TC1060TT2803C	2021/7/25	2021/7/25	1(1/0)	0	1
C346TC18828TC1060T	2021/7/25	2021/7/25	1(1/0)	0	1
C346TC2623T	2021/7/23	2021/7/23	1(0/1)	0	1
C346TC28687T	2021/7/20	2021/7/20	1(1/0)	0	1
C346TC8772T	2021/7/19	2021/7/27	6(3/3)	1	5
C346TG11083T	2021/7/20	2021/7/26	5(3/2)	0	5
C346TG28209T	2021/7/19	2021/7/25	2(1/1)	0	2
C346TG28209TA25934C	2021/7/22	2021/7/29	3(2/1)	1	2
C346TG28209TA25934CC17822T	2021/8/3	2021/8/5	2(2/0)	2	0
C346TG28209TA25934CT7513C	2021/7/31	2021/7/31	1(1/0)	1	0
C346TC8772TG5629T	2021/7/28	2021/7/28	1(1/0)	1	0

C398T	2021/7/26	2021/7/26	1(1/0)	0	1
G167T	2021/7/26	2021/7/26	1(1/0)	0	1
G20995T	2021/7/26	2021/7/26	1(1/0)	0	1
G6865T	2021/7/25	2021/7/25	1(1/0)	0	1
T15567C	2021/7/23	2021/7/30	3(2/1)	1	2
T20751C	2021/7/26	2021/8/1	3(3/0)	3	0
T22738C	2021/7/21	2021/7/21	1(1/0)	0	1
T26259C	2021/7/16	2021/7/22	2(0/2)	0	2
T26259CC1385T	2021/7/20	2021/7/24	2(1/1)	0	2
T26259CG472A	2021/8/6	2021/8/8	2(2/0)	2	0
T26259CG472AC16192A	2021/8/11	2021/8/11	1(1/0)	1	0
T26259CG246T	2021/7/21	2021/7/21	1(1/0)	0	1
A13566G	2021/7/22	2021/7/22	1(0/1)	0	1
C22642TT2803CA15201GC14573TC14576GG26951CT14562C	2021/7/21	2021/7/21	1(0/1)	0	1
C346TC22642T	2021/7/19	2021/7/19	1(0/1)	0	1
T2803CC25452TC25433TC25572T	2021/7/30	2021/7/30	1(0/1)	1	0
T2803CG23868T	2021/7/26	2021/7/26	1(1/0)	0	1
T2803CT7513C	2021/7/29	2021/8/10	2(2/0)	2	0
C13517T	2021/7/26	2021/7/26	1(0/1)	0	1

Combination of Mutation: The emergence of Combination of Mutation in Nanjing.

Date of occurrence of first case: Date of the earliest case among the cases with the Combination of Mutation.

Date of occurrence of last case: Date of the last case among the cases with the Combination of Mutation.

Total number of cases (controlled/uncontrolled): total number of cases of this mutation combination in Nanjing.

Controlled number: onset date of cases after NPI measures (include same date). uncontrolled number: onset date of cases before NPI measures.

Number of cases in control period: Number of cases with onset dates in CI and ER stage.

Number of cases in uncontrolled period: Number of cases with onset dates in NE and II.

Extended data Table 4 | Mutation Combinations of Yangzhou.

Combination of Mutation	Date of onset of first case	Date of onset of last case	Total number of cases (controlled /uncontrolled)	Number of cases in control period	Number of cases in uncontrolled period
T2803CC2939T	2021/7/26	2021/8/1	6(4/2)	6	0
C22642TT2803CG5629T	2021/8/9	2021/8/9	1(0/1)	0	1
G11083TT2803C	2021/8/10	2021/8/10	1(0/1)	0	1
G11083TT2803CC23525T	2021/8/10	2021/8/11	2(1/1)	0	2
G11083TT2803CT7513CC18486TG10533T	2021/7/30	2021/7/30	1(0/1)	1	0
T2803CC5497T	2021/8/6	2021/8/6	1(1/0)	1	0
T2803CG3880A	2021/8/9	2021/8/10	3(1/2)	0	3
T2803C	2021/7/23	2021/8/25	140(75/65)	95	45
T2803CA15201GG26951C	2021/8/5	2021/8/13	4(3/1)	2	2
T2803CA15201GG26951CG26754T	2021/8/10	2021/8/10	1(0/1)	0	1
T2803CA15201GG26951CG26754TG28514T	2021/8/16	2021/8/16	1(0/1)	0	1
T2803CA3908GC19955TA156G	2021/8/11	2021/8/11	1(1/0)	0	1
T2803CA5289T	2021/8/8	2021/8/8	1(1/0)	0	1
T2803CA3908G	2021/7/31	2021/8/13	11(8/3)	5	6
T2803CA3908GG4399T	2021/8/4	2021/8/7	2(1/1)	2	0
T2803CA3908GG5953T	2021/8/7	2021/8/7	1(1/0)	1	0
T2803CA7300T	2021/7/30	2021/8/6	4(3/1)	4	0
T2803CC13329T	2021/8/8	2021/8/11	3(3/0)	0	3
T2803CC13329TC28313T	2021/8/10	2021/8/10	1(1/0)	0	1
T2803CC14573TC14576GC2939T	2021/7/27	2021/7/27	1(0/1)	1	0
T2803CC14573TC14576GT7513CA27156T	2021/7/28	2021/7/28	1(0/1)	1	0
T2803CC14573TC14576GT14562C	2021/7/26	2021/7/26	1(0/1)	1	0
T2803CC14573TC14576GT14562CC23188GC16114TC23300TC25339TG24413T	2021/7/28	2021/7/28	1(0/1)	1	0
T2803CC14573TC14576GT14562CT7513CC18486TG10533TC23188G	2021/8/4	2021/8/4	1(0/1)	1	0
T2803CC14573TC14576GT14562CT7513CC18687T	2021/8/12	2021/8/12	1(1/0)	0	1
T2803CC14573TC14576GT14562CT7513CC23188GC11663A	2021/8/5	2021/8/5	1(1/0)	1	0
T2803CC14708TC14805T	2021/8/5	2021/8/5	1(1/0)	1	0
T2803CC14805T	2021/8/4	2021/8/12	2(2/0)	1	1
T2803CC14805TG558T	2021/8/13	2021/8/13	1(1/0)	0	1

T2803CC14922T	2021/8/8	2021/8/8	1(1/0)	0	1
T2803CC14922TC17444T	2021/7/31	2021/8/1	2(0/2)	2	0
T2803CC14922TC17444TC21772T	2021/8/2	2021/8/2	1(1/0)	1	0
T2803CC14922TC17444TC23525T	2021/8/8	2021/8/8	1(1/0)	0	1
T2803CC17336T	2021/8/6	2021/8/10	3(1/2)	2	1
T2803CC17410T	2021/8/2	2021/8/10	2(1/1)	1	1
T2803CC1758T	2021/8/13	2021/8/13	4(4/0)	0	4
T2803CC19263T	2021/8/8	2021/8/8	1(1/0)	0	1
T2803CC19488T	2021/8/5	2021/8/6	4(0/2)	4	0
T2803CC19955T	2021/8/4	2021/8/4	1(0/1)	1	0
T2803CC2106T	2021/8/4	2021/8/12	6(6/0)	3	3
T2803CC21575T	2021/8/5	2021/8/10	4(4/0)	2	2
T2803CC22712TC7169T	2021/7/29	2021/7/29	1(0/1)	1	0
T2803CC23248T	2021/8/1	2021/8/10	6(5/1)	3	3
T2803CC23525T	2021/8/2	2021/8/2	1(0/1)	1	0
T2803CC23525TC8616T	2021/8/7	2021/8/8	2(2/0)	1	1
T2803CC23525TT23248A	2021/8/6	2021/8/6	1(0/1)	1	0
T2803CC24912T	2021/8/5	2021/8/10	2(1/1)	1	1
T2803CC2523TC2676T	2021/8/8	2021/8/10	2(1/1)	0	2
T2803CC25452TC12809TC15222T	2021/8/3	2021/8/3	1(1/0)	1	0
T2803CC2571T	2021/7/30	2021/7/30	1(1/0)	1	0
T2803CC27641T	2021/8/8	2021/8/8	1(1/0)	0	1
T2803CC2939TG27703T	2021/8/3	2021/8/3	1(1/0)	1	0
T2803CC29614T	2021/8/13	2021/8/13	1(1/0)	0	1
T2803CC29738T	2021/8/4	2021/8/4	1(0/1)	1	0
T2803CC4901T	2021/8/9	2021/8/9	1(0/1)	0	1
T2803CC5079T	2021/8/7	2021/8/7	1(1/0)	1	0
T2803CC5849T	2021/8/3	2021/8/15	5(3/2)	4	1
T2803CC9170TG1729A	2021/8/5	2021/8/5	1(0/1)	1	0
T2803CG12798A	2021/8/7	2021/8/7	1(1/0)	1	0
T2803CG23282T	2021/8/2	2021/8/2	1(0/1)	1	0
T2803CG23501T	2021/8/8	2021/8/8	1(0/1)	0	1
T2803CG23501TG21372T	2021/8/10	2021/8/10	1(0/1)	0	1

T2803CG26389T	2021/7/30	2021/7/30	1(1/0)	1	0
T2803CG26389TG942A	2021/8/6	2021/8/8	2(2/0)	1	1
T2803CG26951C	2021/8/2	2021/8/2	1(0/1)	1	0
T2803CG26951CA27010C	2021/8/6	2021/8/6	1(1/0)	1	0
T2803CG295T	2021/8/11	2021/8/11	1(0/1)	0	1
T2803CG3109T	2021/8/11	2021/8/11	1(1/0)	0	1
T2803CG558T	2021/8/7	2021/8/7	1(1/0)	1	0
T2803CT25518G	2021/8/10	2021/8/10	1(0/5)	0	1
T2803CT7378C	2021/8/7	2021/8/7	1(0/1)	1	0
T2803CT7513C	2021/7/24	2021/8/9	47(28/19)	42	5
T2803CT7513CA27156T	2021/8/12	2021/8/12	1(1/0)	0	1
T2803CT7513CA5458GC2143T23641AT26972C	2021/8/7	2021/8/7	1(0/1)	1	0
T2803CT7513CA655G	2021/8/5	2021/8/5	1(1/0)	1	0
T2803CT7513CC1758T	2021/8/2	2021/8/2	1(1/0)	1	0
T2803CT7513CC18486TG10533T	2021/7/24	2021/8/8	8(5/3)	7	1
T2803CT7513CC18486TG10533TC13176T	2021/8/7	2021/8/7	1(1/0)	1	0
T2803CT7513CC18687T	2021/8/5	2021/8/5	1(1/0)	1	0
T2803CT7513CC22735T	2021/8/9	2021/8/9	1(0/1)	0	1
T2803CT7513CC275A	2021/7/30	2021/7/31	2(2/0)	2	0
T2803CT7513CC2947T	2021/7/26	2021/7/26	1(0/1)	1	0
T2803CT7513CC5147TC5385TG1018A	2021/8/13	2021/8/15	2(2/0)	0	2
T2803CT7513CC6807T	2021/7/26	2021/8/4	4(3/1)	4	0
T2803CT7513CG23282TC29358T	2021/8/4	2021/8/7	2(0/2)	2	0
T2803CT7513CG24577TG25186T	2021/7/29	2021/8/1	4(3/1)	4	0
T2803CT7513CG29645T	2021/8/16	2021/8/16	1(0/1)	0	1
T2803CT7513CG29781T	2021/8/7	2021/8/12	5(2/1)	2	3
T2803CT7513CT694A	2021/8/5	2021/8/5	1(1/0)	1	0

Combination of Mutation: The emergence of Combination of Mutation in Yangzhou.

Time of occurrence of first case: Date of the earliest case among the cases with the Combination of Mutation.

Time of occurrence of last case: Date of the last case among the cases with the Combination of Mutation.

Total number of cases (controlled/uncontrolled): total number of cases of this mutation combination in Yangzhou.

Controlled number: onset date of cases after NPI measures (include same date). uncontrolled number: onset date of cases before NPI measures).

Number of cases in control period: Number of cases with onset dates in CI and ER stage.

Number of cases in uncontrolled period: Number of cases with onset dates in NE and II.

261 **Extended data Table 5 | Summary table of Nanjing-Major combinations of mutations.**

Nanjing—Major combinations of mutations	Number of cases	DATE (First case)	DATE (Last case)
35basic mutation (Common)	51	2021/7/13	2021/7/31
35basic mutation+1 iSNV(Ex346/2803)(Rare)	12	2021/7/20	2021/8/2
35basic mutation+2 iSNV(Ex346/2803)(Rare)	2	2021/7/20	2021/7/30
35basic mutation+3 iSNV(Ex346/2803)(Rare)	1	2021/8/11	2021/8/11
35basic mutation+4 iSNV(Ex346/2803)(Rare)	1	2021/7/26	2021/7/26
35basic mutation+1 iSNV(Ex346/2803)(Common)	16	2021/7/16	2021/8/1
35basic mutation+2 iSNV(Ex346/2803)(Common)	6	2021/7/20	2021/8/8
35basic mutation+C346T(Common)	14	2021/7/13	2021/7/27
35basic mutation+C346T+1 iSNV(Ex2803)(Rare)	3	2021/7/19	2021/7/23
35basic mutation+C346T+2 iSNV(Rare)	4	2021/7/25	2021/7/29
35basic mutation+C346T+3 iSNV(Ex2803)(Rare)	1	2021/7/31	2021/7/31
35basic mutation+C346T+C1060T(Common)	9	2021/7/20	2021/7/25
35basic mutation+C346T+C8772T(Common)	6	2021/7/19	2021/7/27
35basic mutation+C346T+G28209T(Common)	2	2021/7/19	2021/7/25
35basic mutation+C346T+G11083T(Common)	5	2021/7/20	2021/7/26
35basic mutation+C346T+A25934C(Common)	3	2021/7/22	2021/7/29
35basic mutation+C346T+A6411G(Common)	2	2021/7/20	2021/7/23
35basic mutation+C346T+G28209T+A25934C+C17822T(Common)	2	2021/8/3	2021/8/5
35basic mutation+T2803C(Common)	19	2021/7/29	2021/7/31
35basic mutation+T2803C+1 iSNV(Ex346)(Rare)	2	2021/7/26	2021/7/28
35basic mutation+T2803C+3 iSNV(Ex346)(Rare)	1	2021/7/30	2021/7/30
35basic mutation+T2803C+6 iSNV(Ex346)(Rare)	1	2021/7/21	2021/7/21
35basic mutation+T2803C+G16968T(Common)	2	2021/7/28	2021/8/2
35basic mutation+T2803C+T7513C(Common)	2	2021/7/29	2021/8/10

262 Rare: Indicates that the same mutation combination occurs in only one case.
263 Common: Indicates that the same mutation combination occurs in multiple cases.
264 DATE (First case) : is the onset time of the first case of this mutation combination.
265 DATE (Last case) : is the onset time of the last case of this mutation combination.
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Extended data Table 6 | Summary table of Yangzhou-Major combinations of mutations.

Yangzhou-Major combinations of mutations	Number of cases	DATE (First case)	DATE (Last case)
35basic mutation+T2803C (Common)	137	2021/7/23	2021/8/25
35basic mutation+T2803C+1 iSNV(Rare)	23	2021/7/30	2021/8/13
35basic mutation+T2803C+2 iSNV(Rare)	19	2021/7/26	2021/8/16
35basic mutation+T2803C+3 iSNV(Rare)	6	2021/7/26	2021/8/10
35basic mutation+T2803C+4 iSNV(Rare)	5	2021/7/27	2021/8/16
35basic mutation+T2803C+5 iSNV(Rare)	3	2021/7/28	2021/8/12
35basic mutation+T2803C+6 iSNV(Rare)	1	2021/8/5	2021/8/5
35basic mutation+T2803C+7 iSNV(Rare)	1	2021/8/4	2021/8/4
35basic mutation+T2803C+8 iSNV(Rare)	1	2021/7/28	2021/7/28
35basic mutation+T2803C+C14805T(Common)	2	2021/8/4	2021/8/12
35basic mutation+T2803C+C17336T(Common)	2	2021/8/6	2021/8/10
35basic mutation+T2803C+C17410T(Common)	2	2021/8/2	2021/8/10
35basic mutation+T2803C+G3880A(Common)	3	2021/8/9	2021/8/9
35basic mutation+T2803C+C13329T(Common)	3	2021/8/8	2021/8/11
35basic mutation+T2803C+A7300T(Common)	4	2021/7/30	2021/8/6
35basic mutation+T2803C+C1758T(Common)	4	2021/8/13	2021/8/13
35basic mutation+T2803C+C19488T(Common)	4	2021/8/5	2021/8/6
35basic mutation+T2803C+C21575T(Common)	4	2021/8/5	2021/8/10
35basic mutation+T2803C+C5849T(Common)	5	2021/8/3	2021/8/15
35basic mutation+T2803C+C2106T(Common)	6	2021/8/4	2021/8/12
35basic mutation+T2803C+C23248T(Common)	6	2021/8/1	2021/8/10
35basic mutation+T2803C+C2939T(Common)	6	2021/7/26	2021/8/1
35basic mutation+T2803C+A3908G(Common)	11	2021/7/31	2021/8/13
35basic mutation+T2803C+T7513C(Common)	45	2021/7/24	2021/8/9
35basic mutation+T2803C+A21987G(Common)	3	2021/7/29	2021/8/9
35basic mutation+T2803C+C24912T(Common)	2	2021/8/5	2021/8/10
35basic mutation+T2803C+T7513C+C275A(Common)	2	2021/7/30	2021/7/31
35basic mutation+T2803C+T7513C+C6807T(Common)	4	2021/7/26	2021/8/4
35basic mutation+T2803C+T7513C+A21987G(Common)	2	2021/7/28	2021/8/3
35basic mutation+T2803C+T7513C+G29781T(Common)	5	2021/8/7	2021/8/12
35basic mutation+T2803C+G11083T+C23525T(Common)	2	2021/8/10	2021/8/11

35basic mutation+T2803C+A15201G+G26951C(Common)	4	2021/8/5	2021/8/13
35basic mutation+T2803C+A3908G+G4399T(Common)	2	2021/8/4	2021/8/7
35basic mutation+T2803C+C14922T+C17444T(Common)	2	2021/7/31	2021/8/1
35basic mutation+T2803C+C23525T+C8616T(Common)	2	2021/8/7	2021/8/8
35basic mutation+T2803C+C2523T+C2676T(Common)	2	2021/8/8	2021/8/10
35basic mutation+T2803C+G26389T+G942A(Common)	2	2021/8/6	2021/8/8
35basic mutation+T2803C+T7513C+C18486T+G10533T(Common)	8	2021/7/24	2021/8/8
35basic mutation+T2803C+T7513C+G23282T+C29358T(Common)	2	2021/8/4	2021/8/7
35basic mutation+T2803C+T7513C+G24577T+G25186T(Common)	4	2021/7/29	2021/8/1
35basic mutation+T2803C+T7513C+C5147T+C5385T+G1018A(Common)	2	2021/8/13	2021/8/15

Rare: Indicates that the same mutation combination occurs in only one case.

Common: Indicates that the same mutation combination occurs in multiple cases.

DATE (First case): is the onset time of the First case of this mutation combination.

DATE (Last case): is the onset time of the last case of this mutation combination.

Extended data Table 7 | SNV combinations can be terminated by NPI and vaccine.

Variables	Non-Last Patient(case/total) n=371	Last Patient(case/total) n=149	Univariable analysis		Multivariable analysis	
			Odds ratio (95% CI)	<i>p</i> value	Odds ratio (95% CI)	<i>p</i> value
Onset Period						
NE	90(24.3%)	13(8.7%)	Ref	..	Ref	..
II	188(50.7%)	62(41.6%)	2.283(1.194-4.367)	0.013	2.467(1.277-4.764)	0.007
CI	90(24.3%)	67(45%)	5.154(2.659-9.991)	<0.001	5.774(2.931-11.374)	<0.001
ER	3(0.8%)	7(4.7%)	16.154(3.706-70.413)	<0.001	16.118(3.616-71.836)	<0.001
Vaccination						
No	235(63.3%)	83(55.7%)	Ref	..	Ref	..
Vaccinated<30days	98(26.4%)	40(26.8%)	1.156(0.741-1.803)	0.524	1.113(0.701-1.769)	0.649
Vaccinated≥30days	38(10.2%)	26(17.4%)	1.937(1.109-3.385)	0.02	2.33(1.281-4.236)	0.006
Age						
<18	48(12.9%)	21(14.1%)	Ref	..	..	..
[18-30)	32(8.6%)	12(8.1%)	0.857(0.371-1.983)	0.719	NI†	
[30-40)	44(11.9%)	22(14.8%)	1.143(0.554-2.358)	0.718	NI†	
[40-50)	55(14.8%)	32(21.5%)	1.33(0.679-2.607)	0.406	NI†	
[50-60)	66(17.8%)	26(17.4%)	0.9(0.454-1.786)	0.764	NI†	
≥60	126(34%)	36(24.2)	0.653(0.347-1.229)	0.187	NI†	
Sex						
Woman	220(59.3%)	77(51.7%)	Ref	..	..	..
Man	151(40.7%)	72(48.3%)	1.362(0.93-1.997)	0.113	NI†	
CT						
<20	72(19.4%)	36(24.2%)	Ref	..	..	..
[20-30)	194(52.3%)	74(49.7%)	0.763(0.471-1.235)	0.271	NI†	
≥30	105(28.3%)	39(26.2%)	0.743(0.431-1.279)	0.284	NI†	

Clustering						
Nonclustered	149(40.2%)	66(44.3%)	Ref	..	..	..
Clustered	222(59.8%)	83(55.7%)	0.844(0.575-1.239)	0.387	NI†	
Clinical						
Mild	71(19.1%)	31(20.8%)	Ref	..	..	..
Moderate	269(72.5%)	114(76.5%)	0.971(0.603-1.561)	0.902	NI†	
Severe+Critical	31(8.4%)	4(2.7%)	0.296(0.096-0.909)	0.033	NI†	
Termination codon				..	..	..
No	367(98.9%)	145(97.3)	Ref		NI†	
Yes	4(1.1%)	4(2.7%)	2.531(0.625-10.255)	0.193	NI†	

Univariable and multivariable analysis of factors affecting the termination of iSNV mutation combinations.

Vaccination: No = Unvaccinated persons were defined as those who had not been vaccinated and those who had less than 14 days between the time of last vaccination and the time of illness.

Yes = Vaccinations were defined as those who were vaccinated and the interval between the last dose of vaccination and the onset of illness was 14 days or more.

NI†= These factors were not included in the multivariable analysis.

282 **Extended data Table 8 | Demographic characteristics of COVID-19 cases in Nanjing and Yangzhou.**

Demographic data		Cases in Nanjing (n=221)	Cases in Yangzhou (n=559)
Age	<30	42 (19.00%)	125 (22.36%)
	[30-40)	34 (15.38%)	65 (11.63%)
	[40-50)	68 (30.77%)	57 (10.20%)
	[50-60)	48 (21.72%)	87 (15.56%)
	≥60	29 (13.12%)	225 (40.25%)
Sex	Man	85 (38.50%)	237 (42.40%)
	Woman	136 (61.50%)	322 (57.60%)
CT Value	<20	57 (25.79%)	91 (16.28%)
	[20-30)	100 (45.25%)	276 (49.37%)
	≥30	51 (23.08%)	190 (33.99%)
	unknown	13 (5.88%)	2 (0.36%)
Clustering	Nonclustered	189 (85.52%)	109 (19.50%)
	Clustered	32 (14.48%)	450 (80.50%)
Vaccination	No	105 (47.51%)	379 (67.80%)
	Vaccined<30days	16 (7.24%)	38 (6.80%)
	Vaccined≥30days	100 (45.25%)	142 (25.40%)
Clinical type	Mild	160 (72.40%)	419 (74.96%)
	Moderate	51 (23.08%)	85 (15.21%)
	Severe	1 (0.45%)	19 (3.40%)
	Critical	9 (4.07%)	36 (6.44%)

283 Results are expressed as median [minimum and maximum values) and n (%).

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Extended data Table 9 | Key reagents.

REAGENT	SOURCE	IDENTIFIER
SuperScript™ IV First-Strand Synthesis System	Thermo Fisher,USA	Cat# 18091050
Q5® Hot Start High-Fidelity 2X Master Mix	NEB,USA	Cat# M0494S
Long Fragment Target Capture Kit for SARS-CoV-2 Whole Genome	BAIYTECH,China	Cat# BK-LFWCoV024
Target Capture Kit for SARS-CoV-2 Whole Genome	BAIYTECH,China	Cat# BK-WCoV024
TruePrep DNA Library Prep Kit V2 for Illumina	Vazyme,China	Cat# TD502-02
TruePrep index Kit V2 for Illumina	Vazyme,China	Cat# TD202
PhiX Control v3 Support	Illumina,USA	Cat# FC-110-3001
MiSeq™ Reagent Kit v2 (300-cycles)	Illumina,USA	Cat# MS-102-2002
ATOPlex RNA Multiplex PCR-based Library Preparation Set V3.0	MGI,China	Cat# 940-000133-00
MGIEasy Fast PCR-FREE FS Library Prep Set	MGI,China	Cat# 940-000021-00
DNBSEQ one-step	MGI,China	Cat# 1000026466
MGISEQ-2000RS High-throughput Sequencing Set (FCS SE100)	MGI,China	Cat# 1000020570
CPAS Barcode Primer 4 Reagent Kit	MGI,China	Cat# 1000014048
Agilent High Sensitivity DNA Kit	Agilent,USA	Cat# 5067-4626
NGS Reverse Transcription Kit	ABI,USA	Cat# A45003
Ion AmpliSeq SARS-CoV-2 Insight Research Assay - GS Chef-Ready	ABI,USA	Cat# A51306
Ion Torrent™ Ion Library TaqMan™ Quantitation Kit	ABI,USA	Cat# 4468802
Ion 530™ Chip Kit (2 × 4-pack)	ABI,USA	Cat# A27764
Ion 510™ & Ion 520™ & Ion 530™ Kit – Chef (200bp, 2 sequencing run per initialization)	ABI,USA	Cat# A34461
High Pure PCR Product Purification Kit	Roche,New Zealand	Cat# 11732668001
Agencourt AMPure XP	Beckman,USA	Cat# A63881
Qubit™ dsDNA HS Assay Kit	Thermo Fisher,USA	Cat# Q32851
Qubit™ dsDNA BR Assay Kit	Thermo Fisher,USA	Cat# Q32850
Qubit RNA HS Assay Kit	Thermo Fisher,USA	Cat# Q32852
ULSEN Ultra-sensitive Novel Coronavirus Whole-genome capture Kit	MicroFuture,China	Cat# V-090418-1
Nextera DNA Flex Library Prep	Illumina,USA	Cat# 20018704
NXTR® XT DNA SMP Prep Kit	Illumina,USA	Cat# 15032785

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IDT® for Illumina DNA/RNA Unique Dual Indexes Set B	Illumina,USA	Cat# 20027214
IDT® for Illumina DNA/RNA Unique Dual Indexes Set D	Illumina,USA	Cat# 20027216
NextSeq2000 P2 reagent (300 cycle)	Illumina,USA	Cat# 20046813
iseq100 Reagent V2 (300 cycle)	Illumina,USA	Cat# 20031371
MiniSeq Mid Output Kit (300-cycles)	Illumina,USA	Cat# 15073757
Nextera DNA CD Indexes (24 Indexes)	Illumina,USA	Cat# 20018707

Extended data Table 10 | Sample and sequencing information. Related to Figure 1C.

patient_id	sample_id	symptom_onset_date	collection_date	Periods	symptom	sample_type	Prefecture	experiment_type	sequencing_platform	Ct-ORF	Ct-N	mapped_reads	coverage	depth
NJ001	NJ001	2021/7/19	2021/7/21	NE	Mild	OPS	NJ	multiplex-pcr	BGI	26.9	26.1	5,893,109	100.00%	19715.99
NJ002	NJ002	2021/7/16	2021/7/21	NE	Mild	OPS	NJ	multiplex-pcr	BGI	20.55	19.24	5,891,515	100.00%	19710.66
NJ003	NJ003	2021/7/20	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	27.3	26.6	1,414,576	99.56%	5493.016
NJ004	NJ004	2021/7/15	2021/7/21	NE	Mild	OPS	NJ	multiplex-pcr	Illumina	35.4	35.3	1,021,122	99.94%	2583.658
NJ005	NJ005	2021/7/20	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	33	33	741,008	99.02%	1782.179
NJ006	NJ006	2021/7/17	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	30.4	28.6	765,024	99.79%	1936.053
NJ007	NJ007	2021/7/18	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	33.3	32.1	856,100	99.41%	2360.713
NJ009	NJ009	2021/7/20	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	31.4	32.1	5,395,751	100.00%	18052.03
NJ010	NJ010	2021/7/15	2021/7/21	NE	Mild	OPS	NJ	multiplex-pcr	Illumina	21	20	620,017	99.94%	1597.72
NJ011	NJ011	2021/7/18	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	14	12	566,054	99.94%	1478.998
NJ012	NJ012	2021/7/18	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	18	19	1,040,647	99.77%	4054.291
NJ013	NJ013	2021/7/20	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	31.6	28.3	1,906,595	100.00%	6359.526
NJ014	NJ014	2021/7/19	2021/7/21	NE	Mild	OPS	NJ	multiplex-pcr	BGI	32	34	5,908,269	100.00%	19766.71
NJ015	NJ015	2021/7/20	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	18	16	458,247	99.91%	1205.087
NJ020	NJ020	2021/7/13	2021/7/23	NE	Mild	OPS	NJ	multiplex-pcr	Illumina	14	16	1,491,423	99.94%	4594.292
NJ021	NJ021	2021/7/20	2021/7/23	NE	Mild	OPS	NJ	multiplex-pcr	Illumina	26	26	1,467,781	99.84%	4613.42
NJ022	NJ022	2021/7/20	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	20	22	1,558,870	99.93%	4787.205
NJ023	NJ023	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	31	31	1,070,088	99.43%	3439.416
NJ026	NJ026	2021/7/20	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	30	30	2,991,657	99.90%	9992.143
NJ027	NJ027	2021/7/20	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	24	24	1,903,657	99.84%	5739.518
NJ028	NJ028	2021/7/20	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	33	33	1,199,864	99.87%	2009.471
NJ031	NJ031	2021/7/16	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	33	30	2,167,484	99.79%	6598.661
NJ032	NJ032	2021/7/13	2021/7/21	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	29	26	2,073,507	99.65%	6357.679
NJ033	NJ033	2021/7/19	2021/7/23	NE	Mild	OPS	NJ	multiplex-pcr	Illumina	22	22	1,348,934	99.93%	4229.287
NJ034	NJ034	2021/7/19	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	28	28	2,622,422	99.88%	4391.188
NJ035	NJ035	2021/7/15	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	30	31	1,929,804	99.90%	3230.667
NJ036	NJ036	2021/7/19	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	19	20	1,108,812	99.89%	3555.446

NJ037	NJ037	2021/7/17	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	28	30	1,279,287	99.72%	4013.909
NJ039	NJ039	2021/7/22	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	27	28	1,313,571	99.83%	4214.173
NJ040	NJ040	2021/7/19	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	18	18	1,107,193	99.94%	3582.698
NJ041	NJ041	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	25	25	1,347,369	99.92%	4295.82
NJ042	NJ042	2021/7/21	2021/7/23	NE	Mild	OPS	NJ	multiplex-pcr	Illumina	34	34	21,798,793	99.94%	67072.8
NJ043	NJ043	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	34	34	4,516,308	99.70%	13911.44
NJ044	NJ044	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	17	18	3,198,293	99.87%	9750.579
NJ045	NJ045	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	18	21	3,572,903	99.90%	11934.04
NJ046	NJ046	2021/7/22	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	29	29	1,491,545	99.75%	4432.82
NJ047	NJ047	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	25	25	1,133,726	99.70%	3595.7
NJ048	NJ048	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	27	28	2,209,793	99.89%	6822.537
NJ049	NJ049	2021/7/16	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	23	840,602	99.84%	2390.311
NJ050	NJ050	2021/7/19	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	24	1,007,111	99.74%	2937.674
NJ051	NJ051	2021/7/21	2021/7/23	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	24	1,077,943	99.77%	3129.545
NJ052	NJ052	2021/7/19	2021/7/24	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	20	21	824,837	99.93%	2389.559
NJ053	NJ053	2021/7/21	2021/7/24	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	22	1,184,305	99.94%	3440.324
NJ054	NJ054	2021/7/23	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	28	28	56,997,748	99.91%	172081.2
NJ055	NJ055	2021/7/23	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	26	26	62,093,487	99.83%	188204
NJ056	NJ056	2021/7/22	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	25	25	72,371,458	99.91%	218513.8
NJ058	NJ058	2021/7/23	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	26	25	50,849,240	99.91%	154657.7
NJ059	NJ059	2021/7/18	2021/7/25	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	26	26	46,140,680	99.94%	140927.6
NJ061	NJ061	2021/7/22	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	28	28	64,503,228	99.93%	194482.5
NJ062	NJ062	2021/7/23	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	14	14	49,430,285	99.94%	151133.8
NJ063	NJ063	2021/7/24	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	19	19	76,804,846	99.94%	232420.8
NJ064	NJ064	2021/7/24	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	22	59,360,876	99.94%	180672.5
NJ065	NJ065	2021/7/23	2021/7/25	II	Mild	OPS	NJ	multiplex-pcr	Illumina	26	26	64,107,364	99.94%	194675.3
NJ066	NJ066	2021/7/23	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	16	16	43,046,948	99.94%	132379.2
NJ067	NJ067	2021/7/22	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	20	21	60,190,823	99.94%	183448.2
NJ068	NJ068	2021/7/22	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	20	22	46,339,293	99.94%	140256.7

NJ070	NJ070	2021/7/22	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	18	20	71,347,296	99.94%	216842.6
NJ071	NJ071	2021/7/24	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	17	17	47,620,887	99.94%	145410.3
NJ073	NJ073	2021/7/22	2021/7/25	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	33	33	1,716,750	99.94%	5737.751
NJ074	NJ074	2021/7/22	2021/8/8	NE	Moderate	OPS	NJ	multiplex-pcr	Illumina	30	30	435,812	99.65%	1766.879
NJ075	NJ075	2021/7/21	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	24	26	15,848,415	99.91%	58279.28
NJ078	NJ078	2021/7/23	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	32	34	8,925,398	99.88%	31245.42
NJ079	NJ079	2021/7/25	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	34	36	10,381,604	99.92%	32105.38
NJ080	NJ080	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	24	26,219,270	99.94%	100515
NJ082	NJ082	2021/7/22	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	17	23	16,428,932	99.94%	64312.04
NJ084	NJ084	2021/7/23	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	17	23	28,543,584	99.94%	111964.9
NJ085	NJ085	2021/7/21	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	17	22	18,836,610	99.94%	73941.13
NJ086	NJ086	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	23	25	32,857,352	99.94%	127995.6
NJ087	NJ087	2021/7/22	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	19	21	49,255,674	99.94%	190979.2
NJ088	NJ088	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	15	17	38,257,880	99.94%	150158.5
NJ089	NJ089	2021/7/23	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	32	23	5,358,593	99.88%	19284.6
NJ090	NJ090	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	21	25	29,846,203	99.94%	116494.4
NJ091	NJ091	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	21	24	9,941,793	99.94%	39078.62
NJ092	NJ092	2021/7/24	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	24	27	12,788,936	99.94%	49801.79
NJ093	NJ093	2021/7/23	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	24	15,893,058	99.94%	57446.12
NJ094	NJ094	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	22	22	8,984,801	99.94%	34554.35
NJ095	NJ095	2021/7/25	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	16	18	15,173,624	99.94%	58000.42
NJ096	NJ096	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	14	17	9,733,624	99.94%	36982.72
NJ097	NJ097	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	23	24	11,363,700	99.94%	42677.63
NJ098	NJ098	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	32	34	12,737,216	99.93%	46090.27
NJ099	NJ099	2021/7/25	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	18	21	10,816,901	99.91%	41025.49
NJ100	NJ100	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	28	29	23,993,151	99.88%	92676.05
NJ101	NJ101	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	15	18	9,730,420	99.94%	36687.12
NJ102	NJ102	2021/7/25	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	17	17	12,225,834	99.94%	47861.34
NJ103	NJ103	2021/7/19	2021/7/26	NE	Moderate	OPS	NJ	multiplex-pcr	BGI	22	22	2,618,222	99.94%	5256.675

NJ104	NJ104	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	19	21	8,980,819	99.94%	34307.58
NJ105	NJ105	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	30	32	15,530,829	99.85%	53571.21
NJ106	NJ106	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	16	16	14,215,135	99.94%	52387.41
NJ107	NJ107	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	16	19	12,906,137	99.94%	47243.8
NJ110	NJ110	2021/7/25	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	31	31	10,273,633	99.88%	30893.7
NJ114	NJ114	2021/7/24	2021/7/27	II	Mild	OPS	NJ	multiplex-pcr	Illumina	20	19	4,177,539	99.94%	11840.62
NJ115	NJ115	2021/7/26	2021/7/27	II	Mild	OPS	NJ	multiplex-pcr	Illumina	34	32	1,381,603	99.75%	3748.584
NJ120	NJ120	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	28.8	25.9	933,030	99.55%	3555.006
NJ121	NJ121	2021/7/22	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	BGI	38.7	35.9	94,759	99.65%	316.3816
NJ124	NJ124	2021/7/22	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	18.2	15.3	368,032	99.80%	12.33765
NJ125	NJ125	2021/7/23	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	20.4	17.5	640,625	99.61%	1929.753
NJ126	NJ126	2021/7/26	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	15.7	13.2	347,775	99.59%	1013.313
NJ127	NJ127	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	30	29	18,652,075	99.94%	67441.5
NJ129	NJ129	2021/7/26	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	23.4	20.7	1,265,743	99.52%	4981.298
NJ131	NJ131	2021/7/25	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	17.7	14.7	956,763	99.64%	2587.101
NJ132	NJ132	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	25	25	16,835,744	99.94%	62428.16
NJ133	NJ133	2021/7/26	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	29	29	15,810,833	99.94%	57493.49
NJ137	NJ137	2021/7/26	2021/8/10	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	26	26	2,232,338	99.85%	7913.897
NJ138	NJ138	2021/7/26	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	23.1	22	264,942	99.54%	1040.55
NJ141	NJ141	2021/7/26	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	18.8	15.6	980,602	99.52%	2828.862
NJ142	NJ142	2021/7/26	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	31	31	5,402,126	99.92%	8195.749
NJ143	NJ143	2021/7/26	2021/8/10	II	Mild	OPS	NJ	multiplex-pcr	TF	34	34	220,922	99.73%	1464.925
NJ145	NJ145	2021/7/26	2021/7/31	II	Mild	OPS	NJ	multiplex-pcr	Illumina	22.9	19.5	738,808	99.59%	2284.6
NJ146	NJ146	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	24	20.5	494,037	99.61%	1530.478
NJ152	NJ152	2021/7/26	2021/8/10	II	Moderate	OPS	NJ	multiplex-pcr	TF	25	25	2,030,437	99.80%	13709.94
NJ156	NJ156	2021/7/26	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	24.8	23.4	950,238	99.64%	2868
NJ157	NJ157	2021/7/27	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	33.5	32	1,036,888	99.43%	3196.759
NJ158	NJ158	2021/7/25	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	33.3	31.5	758,709	99.46%	2321.692
NJ159	NJ159	2021/7/27	2021/7/28	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	12	13	7,972,661	99.94%	22378.86

NJ160	NJ160	2021/7/26	2021/7/27	II	Moderate	OPS	NJ	multiplex-pcr	BGI	18	22	4,165,046	99.88%	8368.15
NJ162	NJ162	2021/7/27	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	21.2	19.4	930,888	99.73%	2839.635
NJ164	NJ164	2021/7/26	2021/8/10	II	Moderate	OPS	NJ	multiplex-pcr	Illumina	26	27	206,891	99.45%	811.6303
NJ165	NJ165	2021/7/28	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	20.3	19.3	207,893	99.31%	614.5542
NJ166	NJ166	2021/7/27	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	BGI	36.1	36.7	170,059	99.78%	567.0518
NJ167	NJ167	2021/7/27	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	28.6	29.5	1,994,734	99.56%	7735.701
NJ168	NJ168	2021/7/27	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	29.2	28	1,981,999	99.57%	7442.95
NJ175	NJ175	2021/7/27	2021/7/31	CI	Mild	OPS	NJ	multiplex-pcr	Illumina	25.4	23.9	1,148,512	99.68%	3378.314
NJ176	NJ176	2021/7/27	2021/7/31	CI	Mild	OPS	NJ	multiplex-pcr	Illumina	29.4	27.8	1,615,010	99.52%	6120.011
NJ177	NJ177	2021/7/28	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	29.1	28.1	915,298	99.54%	3627.126
NJ179	NJ179	2021/7/28	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	20.4	18.3	1,348,116	99.78%	4041.57
NJ182	NJ182	2021/7/29	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	27.2	24.6	2,025,271	99.56%	7723.182
NJ184	NJ184	2021/7/28	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	BGI	36.4	35.2	327,835	99.89%	1093.516
NJ186	NJ186	2021/7/29	2021/8/10	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	33	33	24,917	98.92%	100.0977
NJ187	NJ187	2021/7/29	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	21.8	20.8	1,040,421	99.67%	3154.95
NJ188	NJ188	2021/7/28	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	27.9	26.5	1,326,499	99.55%	5174.659
NJ189	NJ189	2021/7/30	2021/7/31	CI	Mild	OPS	NJ	multiplex-pcr	Illumina	27.9	26.4	1,061,889	99.62%	3186.831
NJ192	NJ192	2021/7/30	2021/7/31	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	25.4	23.9	1,508,078	99.60%	5824.268
NJ193	NJ193	2021/7/30	2021/8/10	CI	Mild	OPS	NJ	multiplex-pcr	TF	30	30	2,329,786	99.75%	15682.61
NJ195	NJ195	2021/7/24	2021/7/31	II	Moderate	OPS	NJ	multiplex-pcr	TF	39	39	2,139,455	99.86%	14813.98
NJ196	NJ196	2021/7/28	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	32	30	2,686,673	99.88%	15400.34
NJ197	NJ197	2021/7/30	2021/8/3	CI	Mild	OPS	NJ	multiplex-pcr	TF	25	27	3,707,905	99.89%	25547.63
NJ198	NJ198	2021/7/30	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	26	27	647,062	99.82%	4427.391
NJ199	NJ199	2021/7/31	2021/8/10	CI	Moderate	OPS	NJ	multiplex-pcr	TF	30	30	1,365,684	99.78%	9089.513
NJ200	NJ200	2021/7/31	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	22	24	5,636,384	99.83%	39085.66
NJ201	NJ201	2021/7/31	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	25	27	2,350,858	99.83%	16234.55
NJ203	NJ203	2021/7/30	2021/8/10	CI	Moderate	OPS	NJ	multiplex-pcr	TF	33	33	1,372,493	99.78%	9263.599
NJ204	NJ204	2021/7/28	2021/8/3	CI	Mild	OPS	NJ	multiplex-pcr	TF	23	25	4,055,842	99.85%	28033.93
NJ205	NJ205	2021/7/31	2021/8/3	CI	Mild	OPS	NJ	multiplex-pcr	TF	26	28	1,019,838	99.79%	7040.493

NJ206	NJ206	2021/7/31	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	18	20	5,428,442	99.92%	29739.42
NJ207	NJ207	2021/7/31	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	14	16	5,778,873	99.83%	37018.06
NJ208	NJ208	2021/7/22	2021/8/3	II	Mild	OPS	NJ	multiplex-pcr	TF	32	33	1,654,095	99.82%	10618.64
NJ209	NJ209	2021/7/30	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	24	27	4,016,786	99.84%	25074.3
NJ210	NJ210	2021/7/30	2021/8/3	CI	Mild	OPS	NJ	multiplex-pcr	TF	17	20	3,074,352	99.78%	17238.55
NJ211	NJ211	2021/7/29	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	23	24	3,905,947	99.82%	26785.25
NJ212	NJ212	2021/7/31	2021/8/3	CI	Mild	OPS	NJ	multiplex-pcr	TF	17	15	3,038,581	99.83%	15513.77
NJ213	NJ213	2021/7/31	2021/8/3	CI	Mild	OPS	NJ	multiplex-pcr	TF	37	36	1,195,453	99.56%	5174.975
NJ215	NJ215	2021/7/31	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	31	33	2,874,080	99.87%	18781.26
NJ217	NJ217	2021/7/31	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	13	15	4,053,568	99.92%	24870.71
NJ218	NJ218	2021/8/1	2021/8/10	CI	Moderate	OPS	NJ	multiplex-pcr	TF	28	29	2,451,953	99.79%	16057.24
NJ220	NJ220	2021/7/31	2021/8/3	CI	Moderate	OPS	NJ	multiplex-pcr	TF	15	19	4,713,137	99.84%	30434.29
NJ221	NJ221	2021/8/2	2021/8/10	CI	Moderate	OPS	NJ	multiplex-pcr	TF	30	30	1,979,837	99.78%	13042.76
NJ222	NJ222	2021/7/30	2021/8/6	CI	Moderate	OPS	NJ	multiplex-pcr	TF	18	20	2,912,071	99.67%	16475.41
NJ223	NJ223	2021/7/26	2021/8/6	CI	Mild	NPS	NJ	multiplex-pcr	Illumina	30	30	335,666	98.79%	1037.277
NJ224	NJ224	2021/8/2	2021/8/6	CI	Moderate	NPS	NJ	multiplex-pcr	Illumina	16	19	736,787	99.59%	2887.592
NJ226	NJ226	2021/8/1	2021/8/4	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	35	33	2,021,475	99.76%	7442.81
NJ227	NJ227	2021/8/3	2021/8/4	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	34	33	1,193,633	99.70%	4344.945
NJ228	NJ228	2021/8/4	2021/8/6	CI	Moderate	OPS	NJ	multiplex-pcr	Illumina	38	36	862,254	99.87%	3436.348
NJ229	NJ229	2021/8/5	2021/8/6	ER	Moderate	NPS	NJ	multiplex-pcr	Illumina	36	36	670,441	99.41%	2329.684
NJ230	NJ230	2021/8/6	2021/8/7	ER	Moderate	NPS	NJ	multiplex-pcr	Illumina	19	18	544,726	99.82%	1882.677
NJ232	NJ232	2021/8/8	2021/8/9	ER	Moderate	OPS	NJ	multiplex-pcr	Illumina	24	25	23,233,671	99.93%	90935.46
NJ234	NJ234	2021/8/10	2021/8/14	ER	Moderate	OPS	NJ	multiplex-pcr	Illumina	20	21	1,643,699	99.94%	6532.425
NJ235	NJ235	2021/8/11	2021/8/13	ER	Moderate	OPS	NJ	multiplex-pcr	BGI	28	26	12,826,523	99.93%	40712.12
YZ001	YZ001	2021/7/23	2021/7/28	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	19	20	2,712,182	99.92%	7319.275
YZ002	YZ002	2021/7/25	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	16	16	58,468,029	99.93%	165219.4
YZ003	YZ003	2021/7/25	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	18	18	36,241,018	99.92%	100101.2
YZ004	YZ004	2021/7/27	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	18	18	8,596,632	99.92%	17094.83
YZ005	YZ005	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	18	18	32,763,885	99.94%	90837.97

YZ006	YZ006	2021/7/25	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	18	19	9,629,323	99.87%	23400.49
YZ007	YZ007	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	30	52,444,838	99.93%	137320
YZ009	YZ009	2021/7/25	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	18	14	69,834,847	99.92%	177166.5
YZ010	YZ010	2021/7/27	2021/8/10	NE	Severe	OPS	YZ	multiplex-pcr	Illumina	26	26	1,347,834	99.30%	5408.447
YZ012	YZ012	2021/7/26	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	20	18	44,594,971	99.92%	113449
YZ013	YZ013	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	18	18	57,395,337	99.92%	153102.3
YZ014	YZ014	2021/7/29	2021/8/2	NE	Critical	OPS	YZ	multiplex-pcr	Illumina	36	34	64,707,878	99.92%	176122.7
YZ015	YZ015	2021/7/28	2021/8/2	NE	Critical	OPS	YZ	multiplex-pcr	Illumina	28	28	26,392,447	99.92%	54900.49
YZ016	YZ016	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	17	17	2,917,680	99.94%	10812.31
YZ018	YZ018	2021/7/29	2021/8/2	NE	Moderate	NPS	YZ	multiplex-pcr	Illumina	16	16	15,010,240	99.87%	55382.95
YZ019	YZ019	2021/7/29	2021/8/4	NE	Severe	OPS	YZ	multiplex-pcr	TF	30	31	1,779,230	99.75%	12514.63
YZ020	YZ020	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	18	18	2,227,180	99.94%	8663.303
YZ021	YZ021	2021/7/24	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	30	16,018,498	99.94%	62475.28
YZ023	YZ023	2021/7/26	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	14	12	13,963,501	99.94%	54454.75
YZ025	YZ025	2021/7/29	2021/8/2	NE	Mild	OPS	YZ	multiplex-pcr	Illumina	26	26	2,812,766	99.93%	10640.39
YZ026	YZ026	2021/7/24	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	28	26	2,584,161	99.94%	9893.152
YZ029	YZ029	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	16	16	21,371,244	99.94%	82914.15
YZ030	YZ030	2021/7/30	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	30	30	611,093	99.77%	1479.57
YZ031	YZ031	2021/7/30	2021/8/2	II	Critical	OPS	YZ	multiplex-pcr	BGI	28	27	7,674,117	99.87%	18306.22
YZ032	YZ032	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	30	28	1,875,242	99.82%	4569.217
YZ033	YZ033	2021/7/30	2021/8/4	NE	Moderate	OPS	YZ	multiplex-pcr	TF	30	29	3,253,177	99.81%	19820.28
YZ034	YZ034	2021/7/30	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	24	25	9,561,798	99.87%	23011.31
YZ035	YZ035	2021/7/28	2021/8/2	NE	Critical	OPS	YZ	multiplex-pcr	BGI	33	33	4,420,638	99.76%	10363.18
YZ036	YZ036	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	11	13	3,511,111	99.87%	8343.174
YZ037	YZ037	2021/7/30	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	24	24	21,821,627	99.94%	85312.91
YZ038	YZ038	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	20	20	2,683,209	99.94%	10163.03
YZ039	YZ039	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	36	32	17,285,078	99.94%	66818.34
YZ041	YZ041	2021/7/30	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	16	14	9,218,644	99.90%	35912.87
YZ043	YZ043	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	20	20	10,396,251	99.93%	39480.57

YZ044	YZ044	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	22	22	15,465,439	99.94%	60372.59
YZ045	YZ045	2021/7/28	2021/8/2	NE	Critical	OPS	YZ	multiplex-pcr	Illumina	22	22	11,045,899	99.93%	42928.45
YZ046	YZ046	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	26	26	8,661,265	99.94%	34165.79
YZ047	YZ047	2021/7/30	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	26	26	8,709,930	99.94%	33456.66
YZ048	YZ048	2021/7/29	2021/8/2	NE	Mild	OPS	YZ	multiplex-pcr	BGI	35	34	128,185	99.75%	305.8903
YZ049	YZ049	2021/7/26	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	18	16	9,749,776	99.94%	37718.75
YZ050	YZ050	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	28	10,313,725	99.94%	40392.38
YZ051	YZ051	2021/7/25	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	15	16	8,365,427	99.87%	19913.8
YZ052	YZ052	2021/7/30	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	24	15,001,500	99.94%	57833.11
YZ053	YZ053	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	26	24	12,749,496	99.94%	49413.07
YZ054	YZ054	2021/7/30	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	32	32	10,703,647	99.94%	42188.11
YZ056	YZ056	2021/7/31	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	29	29.6	1,760,781	99.81%	12293.7
YZ057	YZ057	2021/7/31	2021/8/2	II	Critical	OPS	YZ	multiplex-pcr	BGI	33	33	2,299,706	99.82%	5468.761
YZ058	YZ058	2021/7/31	2021/8/2	II	Severe	OPS	YZ	multiplex-pcr	TF	10	9	6,754,215	99.94%	42702.32
YZ059	YZ059	2021/7/29	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	TF	30.8	29.5	366,294	99.82%	2137.946
YZ060	YZ060	2021/7/28	2021/8/10	NE	Moderate	OPS	YZ	multiplex-pcr	TF	26	26	1,989,538	99.81%	12870.68
YZ061	YZ061	2021/7/31	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	24	25	382,249	99.61%	1520.48
YZ062	YZ062	2021/7/31	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	16	14	5,822,047	99.84%	37460.54
YZ063	YZ063	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	18	20	8,266,380	99.86%	19679.56
YZ064	YZ064	2021/7/31	2021/8/2	II	Mild	OPS	YZ	multiplex-pcr	BGI	12	15	1,059,825	99.47%	2518.665
YZ065	YZ065	2021/8/1	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	37	30	100,167	99.56%	701.6162
YZ066	YZ066	2021/8/1	2021/8/2	II	Mild	OPS	YZ	multiplex-pcr	BGI	25	25	9,546,646	99.87%	23531.25
YZ067	YZ067	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	14	18	8,243,515	99.94%	19534.97
YZ069	YZ069	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	22	23	8,357,344	99.86%	20053.69
YZ070	YZ070	2021/7/28	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	Illumina	20	20	2,417,562	99.94%	9297.844
YZ074	YZ074	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	32	31	1,327,834	99.75%	3175.667
YZ076	YZ076	2021/7/30	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	20	21	11,193,272	99.86%	26883.59
YZ077	YZ077	2021/7/30	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	23	23.5	941,026	99.79%	5562.444
YZ079	YZ079	2021/7/31	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	24.5	25	713,348	99.72%	4244.41

YZ080	YZ080	2021/7/24	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	17	19	18,803,063	99.87%	45081.26
YZ081	YZ081	2021/7/26	2021/8/2	NE	Critical	OPS	YZ	multiplex-pcr	BGI	12	14	7,317,739	99.94%	17501.15
YZ082	YZ082	2021/7/28	2021/8/2	NE	Severe	OPS	YZ	multiplex-pcr	Illumina	37	27	5,224,634	99.94%	20784.64
YZ083	YZ083	2021/7/29	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	28	27	2,795,146	99.83%	19406.64
YZ084	YZ084	2021/7/31	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	14	14	3,967,031	99.89%	25247.41
YZ085	YZ085	2021/8/1	2021/8/10	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	25	26	126,134	99.51%	509.782
YZ086	YZ086	2021/8/1	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	29.8	29.1	1,669,001	99.73%	11025.46
YZ087	YZ087	2021/7/29	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	11	14	3,896,582	99.82%	9265.278
YZ089	YZ089	2021/7/30	2021/8/4	NE	Moderate	OPS	YZ	multiplex-pcr	TF	11.6	15.6	1,036,643	99.78%	6065.386
YZ091	YZ091	2021/8/1	2021/8/18	II	Critical	OPS	YZ	multiplex-pcr	Illumina	33	29	2,361,315	99.86%	9001.676
YZ092	YZ092	2021/7/31	2021/8/4	II	Mild	OPS	YZ	multiplex-pcr	TF	24	24	2,527,051	99.77%	17389.03
YZ094	YZ094	2021/8/1	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	22.8	25	5,262,546	99.77%	36825.15
YZ095	YZ095	2021/7/27	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	15	15	8,457,881	99.86%	20202.7
YZ096	YZ096	2021/7/31	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	28	28	2,439,837	99.68%	14895.12
YZ097	YZ097	2021/7/31	2021/8/2	II	Mild	OPS	YZ	multiplex-pcr	BGI	31	32	868,847	99.79%	2075.863
YZ098	YZ098	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	32	30	533,844	99.76%	1278.872
YZ099	YZ099	2021/8/1	2021/8/4	NE	Moderate	OPS	YZ	multiplex-pcr	TF	26	26	3,620,921	99.77%	23267.64
YZ100	YZ100	2021/8/1	2021/8/4	II	Severe	OPS	YZ	multiplex-pcr	TF	21.5	21	4,584,156	99.83%	26154.21
YZ102	YZ102	2021/7/25	2021/8/2	NE	Severe	OPS	YZ	multiplex-pcr	Illumina	14	15	7,330,743	99.87%	17581.64
YZ103	YZ103	2021/7/31	2021/8/2	II	Severe	OPS	YZ	multiplex-pcr	Illumina	11	13	4,579,104	99.85%	10873.22
YZ104	YZ104	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	24	24	8,290,978	99.87%	19951.34
YZ105	YZ105	2021/7/28	2021/8/4	NE	Critical	OPS	YZ	multiplex-pcr	Illumina	21.7	21.9	2,408,982	99.94%	9570.654
YZ106	YZ106	2021/8/2	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	28.7	29	534,516	99.56%	3070.922
YZ108	YZ108	2021/8/1	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	20	20	10,261,348	99.89%	24982.77
YZ109	YZ109	2021/7/31	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	11	11	5,216,616	99.92%	32975.43
YZ110	YZ110	2021/7/30	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	14	15	13,716,800	99.93%	32766.8
YZ112	YZ112	2021/7/31	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	22	23	15,651,848	99.87%	38105.87
YZ115	YZ115	2021/7/31	2021/8/10	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	25	25	326,364	99.58%	1282.524
YZ118	YZ118	2021/8/2	2021/8/4	II	Mild	OPS	YZ	multiplex-pcr	TF	32.5	29	883,515	98.34%	4288.538

YZ121	YZ121	2021/8/1	2021/8/4	II	Mild	OPS	YZ	multiplex-pcr	Illumina	27.8	27.8	677,644	99.84%	2645.484
YZ124	YZ124	2021/8/1	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	32.7	29	1,820,038	99.38%	7518.475
YZ125	YZ125	2021/7/29	2021/8/2	NE	Mild	OPS	YZ	multiplex-pcr	Illumina	24	24	2,693,751	99.94%	10449.46
YZ126	YZ126	2021/7/30	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	29	28	534,362	99.76%	1323.141
YZ128	YZ128	2021/8/2	2021/8/10	II	Mild	OPS	YZ	multiplex-pcr	TF	23	24	2,725,696	99.77%	18569.52
YZ129	YZ129	2021/8/2	2021/8/10	II	Mild	OPS	YZ	multiplex-pcr	Illumina	20	20	4,735,926	99.94%	18633.52
YZ131	YZ131	2021/8/2	2021/8/19	II	Mild	OPS	YZ	multiplex-pcr	Illumina	15	15	11,921,156	99.94%	47331.99
YZ134	YZ134	2021/8/2	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	25.7	25.4	2,613,281	99.82%	11572.27
YZ135	YZ135	2021/8/3	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	25.4	24.2	2,113,210	99.84%	11769.19
YZ137	YZ137	2021/8/3	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	24	23.4	3,481,957	99.83%	21265.62
YZ140	YZ140	2021/8/2	2021/8/10	II	Critical	OPS	YZ	multiplex-pcr	Illumina	27	27	291,450	99.58%	1163.023
YZ143	YZ143	2021/7/31	2021/8/10	II	Critical	OPS	YZ	multiplex-pcr	Illumina	30	30	355,622	98.97%	1424.866
YZ146	YZ146	2021/8/2	2021/8/10	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	29	30	342,842	99.62%	1364.552
YZ149	YZ149	2021/8/1	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	13	12	3,476,175	99.85%	8265.455
YZ155	YZ155	2021/8/4	2021/8/18	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	30	2,870,743	99.59%	10956.42
YZ156	YZ156	2021/8/3	2021/8/4	II	Moderate	OPS	YZ	multiplex-pcr	TF	28.5	27	4,516,139	99.78%	25690.52
YZ159	YZ159	2021/8/3	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	37	37	2,132,592	99.87%	7965.675
YZ160	YZ160	2021/8/3	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	BGI	35	35	47,442	99.15%	156.0289
YZ161	YZ161	2021/8/2	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	25	28	2,338,350	99.88%	9279.92
YZ162	YZ162	2021/8/3	2021/8/11	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	23	24	14,624,517	99.93%	56873.11
YZ163	YZ163	2021/8/1	2021/8/2	II	Moderate	OPS	YZ	multiplex-pcr	BGI	26	24	19,885,750	99.87%	49195.98
YZ168	YZ168	2021/7/30	2021/8/6	II	Mild	OPS	YZ	multiplex-pcr	Illumina	30	31	1,766,729	99.78%	7074.892
YZ169	YZ169	2021/8/4	2021/8/6	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	31	33	711,115	99.70%	2651.302
YZ170	YZ170	2021/7/30	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	27	29	1,816,118	99.91%	7103.912
YZ171	YZ171	2021/8/4	2021/8/6	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	37	35	13,927,942	99.89%	52769.75
YZ172	YZ172	2021/8/3	2021/8/14	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	36	37	2,395,738	98.56%	8997.583
YZ175	YZ175	2021/8/4	2021/8/5	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	27	29	1,858,767	99.88%	7435.49
YZ178	YZ178	2021/8/3	2021/8/4	II	Moderate	NPS	YZ	multiplex-pcr	TF	25.5	24	2,195,424	99.85%	9906.395
YZ181	YZ181	2021/8/1	2021/8/11	II	Mild	OPS	YZ	multiplex-pcr	BGI	33	33	175,226	99.89%	570.4045

YZ182	YZ182	2021/7/29	2021/8/11	NE	Moderate	NPS	YZ	multiplex-pcr	Illumina	26	28	21,147,871	99.90%	83632.72
YZ187	YZ187	2021/8/3	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	34	34	11,843,814	99.82%	41502.75
YZ188	YZ188	2021/7/31	2021/8/11	II	Severe	NPS	YZ	multiplex-pcr	Illumina	32	32	6,387,839	99.82%	23724.33
YZ192	YZ192	2021/7/31	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	28	28	40,771,872	99.87%	156992.8
YZ196	YZ196	2021/8/2	2021/8/6	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	37	39	520,905	98.99%	1957.041
YZ198	YZ198	2021/7/26	2021/8/2	NE	Critical	NPS	YZ	multiplex-pcr	BGI	20	21	13,806,372	99.85%	33115.98
YZ200	YZ200	2021/7/31	2021/8/2	II	Severe	NPS	YZ	multiplex-pcr	BGI	34	32	128,528	99.74%	310.6324
YZ202	YZ202	2021/8/4	2021/8/6	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	34	35	1,748,828	99.79%	6504.53
YZ204	YZ204	2021/7/31	2021/8/6	II	Severe	NPS	YZ	multiplex-pcr	Illumina	38	37	28,064,559	99.94%	107814.6
YZ210	YZ210	2021/8/4	2021/8/6	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	26	26	1,057,775	99.56%	3941.723
YZ211	YZ211	2021/8/1	2021/8/6	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	33	34	1,008,907	99.36%	3957.272
YZ212	YZ212	2021/8/4	2021/8/6	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	28	27	1,902,567	99.71%	7617.377
YZ214	YZ214	2021/8/5	2021/8/6	II	Mild	OPS	YZ	multiplex-pcr	Illumina	32	33	1,111,334	99.44%	4294.378
YZ215	YZ215	2021/8/3	2021/8/6	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	34	34	2,035,002	99.50%	7912.416
YZ224	YZ224	2021/8/5	2021/8/11	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	33	33	2,073,165	99.52%	8037.804
YZ227	YZ227	2021/8/4	2021/9/23	NE	Moderate	NPS	YZ	multiplex-pcr	Illumina	32	33	2,045,507	99.74%	6873.464
YZ229	YZ229	2021/7/30	2021/8/2	NE	Critical	NPS	YZ	multiplex-pcr	BGI	27	26	12,727,899	99.87%	31022.64
YZ230	YZ230	2021/8/3	2021/8/11	II	Severe	NPS	YZ	multiplex-pcr	Illumina	30	30	8,289,250	99.88%	32209.97
YZ232	YZ232	2021/8/5	2021/8/6	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	34	34	1,143,673	99.83%	4428.969
YZ234	YZ234	2021/8/4	2021/8/6	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	27	24	981,941	99.76%	3879.749
YZ235	YZ235	2021/8/5	2021/8/6	II	Critical	NPS	YZ	multiplex-pcr	Illumina	25	23	482,974	99.57%	1908.759
YZ236	YZ236	2021/8/4	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	32	1,218,309	99.85%	4509.005
YZ240	YZ240	2021/8/5	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	33	6,920,826	99.84%	22568.44
YZ242	YZ242	2021/8/5	2021/8/11	II	Mild	NPS	YZ	multiplex-pcr	Illumina	24	24	23,152,212	99.94%	92512.51
YZ249	YZ249	2021/8/4	2021/8/6	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	22	21	1,351,732	99.56%	5197.615
YZ251	YZ251	2021/8/5	2021/8/18	II	Mild	OPS	YZ	multiplex-pcr	Illumina	30	32	1,862,987	99.90%	6984.405
YZ254	YZ254	2021/8/5	2021/8/11	II	Severe	NPS	YZ	multiplex-pcr	Illumina	31	31	10,806,436	99.93%	40182.28
YZ256	YZ256	2021/8/4	2021/8/18	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	33	34	295,292	99.24%	1116.229
YZ265	YZ265	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	BGI	30	30	373,658	99.89%	1246.48

YZ266	YZ266	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	BGI	18	18	352,353	99.94%	1147.764
YZ268	YZ268	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	BGI	35	35	62,419	99.47%	204.7944
YZ271	YZ271	2021/8/5	2021/8/19	II	Mild	OPS	YZ	multiplex-pcr	Illumina	31	31	3,604,361	99.87%	13824.5
YZ272	YZ272	2021/8/5	8/18/2021	II	Mild	OPS	YZ	multiplex-pcr	Illumina	32	34	18,416,391	99.93%	68807.29
YZ275	YZ275	2021/8/6	2021/8/7	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	19	19	643,515	99.93%	2149.275
YZ278	YZ278	2021/8/1	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	26	27	10,281,151	99.93%	39609.08
YZ279	YZ279	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	33	273,118	99.56%	1024.564
YZ280	YZ280	2021/8/5	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	23	25	17,762,709	99.94%	66302.55
YZ281	YZ281	2021/8/5	2021/8/18	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	29	29	11,088,918	99.94%	41678.39
YZ282	YZ282	2021/8/6	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	14	14	16,938,798	99.94%	64715.86
YZ283	YZ283	2021/8/5	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	17	17	14,419,736	99.94%	56103.2
YZ284	YZ284	2021/8/5	2021/8/18	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	16	17	21,164,008	99.94%	73816.79
YZ285	YZ285	2021/8/6	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	33	1,530,147	99.85%	5789.582
YZ286	YZ286	2021/8/7	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	19	19	14,431,679	99.93%	55292.96
YZ288	YZ288	2021/8/5	2021/8/11	II	Severe	NPS	YZ	multiplex-pcr	Illumina	32	32	2,394,309	99.83%	9104.587
YZ289	YZ289	2021/8/5	2021/8/7	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	31	28	684,518	99.68%	2284.642
YZ290	YZ290	2021/8/6	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	27	27	3,446,589	99.68%	12361.52
YZ291	YZ291	2021/8/6	2021/8/18	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	29	29	2,274,406	99.59%	8934.633
YZ298	YZ298	2021/8/6	2021/8/11	II	Severe	NPS	YZ	multiplex-pcr	Illumina	31	31	19,327,073	99.94%	73727.15
YZ303	YZ303	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	33	33,984,348	99.88%	121622.1
YZ304	YZ304	2021/8/6	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	26	28	24,080,266	99.87%	95047.11
YZ307	YZ307	2021/8/2	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	24	25	13,970,217	99.93%	52657.07
YZ308	YZ308	2021/8/4	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	23	24	2,005,515	99.86%	7927.65
YZ309	YZ309	2021/8/6	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	27	28	1,890,571	99.84%	7555.75
YZ310	YZ310	2021/8/6	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	22	23	1,891,507	99.93%	6243.864
YZ311	YZ311	2021/8/7	2021/8/18	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	27	28	6,626,249	99.88%	25058.76
YZ315	YZ315	2021/8/5	2021/8/11	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	28	28.2	5,013,865	99.90%	18425.42
YZ319	YZ319	2021/8/7	2021/8/8	II	Mild	NPS	YZ	multiplex-pcr	Illumina	27	26	193,330	99.74%	784.58
YZ323	YZ323	2021/8/7	2021/8/8	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	26	26	369,023	99.74%	1455.258

YZ326	YZ326	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	29	30	3,056,235	99.93%	11225.91
YZ328	YZ328	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	21	22	1,731,558	99.94%	6924.178
YZ329	YZ329	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	32	35	350,607	99.75%	1320.504
YZ330	YZ330	2021/8/4	2021/8/19	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	29	29	16,093,247	99.86%	60984.61
YZ331	YZ331	2021/8/2	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	30	30	1,533,060	99.86%	5568.201
YZ334	YZ334	2021/8/7	2021/8/8	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	25	25	189,594	99.56%	759.6693
YZ338	YZ338	2021/8/4	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	20	22	31,980,006	99.94%	124808.9
YZ339	YZ339	2021/8/1	2021/8/11	II	Mild	NPS	YZ	multiplex-pcr	Illumina	32	32	7,882,454	99.82%	29740.9
YZ340	YZ340	2021/8/7	2021/8/8	II	Mild	NPS	YZ	multiplex-pcr	Illumina	22	20	576,961	99.77%	2322.174
YZ341	YZ341	2021/8/8	2021/8/8	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	22	21	607,944	99.58%	2444.163
YZ342	YZ342	2021/8/5	2021/8/18	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	30	30	7,351,180	99.88%	27594.85
YZ343	YZ343	2021/7/25	2021/8/2	NE	Moderate	OPS	YZ	multiplex-pcr	BGI	32	30	395,850	99.83%	954.9447
YZ345	YZ345	2021/8/7	2021/8/9	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	34	38	1,336,398	99.94%	5253.582
YZ348	YZ348	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	20	20	2,809,689	99.94%	11277.17
YZ350	YZ350	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	17	19	16,273,985	99.94%	64186.88
YZ351	YZ351	2021/8/8	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	34	2,479,611	99.07%	9487.248
YZ352	YZ352	2021/8/8	2021/8/11	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	30	30	30,167,034	99.85%	115703.4
YZ353	YZ353	2021/8/6	2021/8/9	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	28	28	2,774,725	99.94%	11161.65
YZ354	YZ354	2021/8/7	2021/8/9	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	34	34	2,138,256	98.99%	7975.334
YZ355	YZ355	2021/8/6	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	17	20	23,935,317	99.94%	91840.22
YZ356	YZ356	2021/8/7	2021/8/9	II	Mild	NPS	YZ	multiplex-pcr	Illumina	32	32	5,717,220	99.90%	19674.22
YZ357	YZ357	2021/8/4	2021/8/11	II	Mild	OPS	YZ	multiplex-pcr	Illumina	32	33	1,362,037	99.81%	5324.623
YZ358	YZ358	2021/8/6	2021/8/9	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	27	27	3,313,288	99.92%	13348.19
YZ360	YZ360	2021/8/7	2021/8/9	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	32	1,670,497	99.82%	5663.923
YZ362	YZ362	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	24	24	30,911,678	99.99%	123339.4
YZ363	YZ363	2021/8/4	2021/8/11	II	Critical	NPS	YZ	multiplex-pcr	Illumina	20	20	21,990,916	99.94%	84499.94
YZ364	YZ364	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	30	31	2,473,670	99.93%	9687.334
YZ365	YZ365	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	21	23	1,407,252	99.90%	5587.949
YZ366	YZ366	2021/8/7	2021/8/9	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	30	30	2,858,406	99.74%	11499.21

YZ367	YZ367	2021/8/7	2021/8/9	II	Mild	OPS	YZ	multiplex-pcr	Illumina	30	30	3,016,439	99.93%	12120.94
YZ368	YZ368	2021/8/8	2021/8/9	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	33	3,379,807	99.83%	13612.13
YZ374	YZ374	2021/8/7	2021/8/11	II	Mild	OPS	YZ	multiplex-pcr	Illumina	32	33	3,008,852	99.86%	11601.56
YZ375	YZ375	2021/8/6	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	24	24	37,152,195	99.94%	140957.5
YZ376	YZ376	2021/8/7	2021/8/12	II	Mild	OPS	YZ	multiplex-pcr	Illumina	26	26	1,456,716	99.29%	5837.734
YZ378	YZ378	2021/8/8	2021/8/11	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	36	35	1,734,739	99.72%	6971.058
YZ380	YZ380	2021/8/4	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	20	20	19,612,173	99.94%	75911.87
YZ381	YZ381	2021/8/8	2021/8/11	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	27	28	1,963,325	99.90%	7867.678
YZ383	YZ383	2021/8/4	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	24	24	23,052,751	99.94%	91010.4
YZ385	YZ385	2021/8/8	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	19	20	14,918,001	99.94%	58514.6
YZ386	YZ386	2021/8/8	2021/8/11	CI	Severe	NPS	YZ	multiplex-pcr	Illumina	26	28	24,948,522	99.94%	97426.32
YZ387	YZ387	2021/8/7	2021/8/12	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	29	28	1,225,594	99.13%	4899.398
YZ388	YZ388	2021/8/8	2021/8/10	CI	Mild	OPS	YZ	multiplex-pcr	TF	29	28	763,636	99.77%	4627.807
YZ391	YZ391	2021/8/8	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	16	18	17,871,746	99.94%	70134.84
YZ392	YZ392	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	26	27	20,039,407	99.94%	79100.37
YZ393	YZ393	2021/8/8	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	24	26	26,345,467	99.84%	103677.7
YZ394	YZ394	2021/8/2	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	32	33	38,343,842	99.88%	134896.5
YZ395	YZ395	2021/8/9	2021/8/11	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	22	25	22,988,304	99.93%	88592.28
YZ396	YZ396	2021/8/8	2021/8/11	CI	Severe	NPS	YZ	multiplex-pcr	Illumina	24	25	23,320,978	99.86%	87800.49
YZ397	YZ397	2021/8/8	2021/8/10	CI	Moderate	OPS	YZ	multiplex-pcr	TF	20	20	2,652,447	99.91%	17511.01
YZ398	YZ398	2021/8/8	2021/8/11	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	31	1,515,258	99.93%	5865.973
YZ399	YZ399	2021/8/7	2021/8/10	II	Moderate	OPS	YZ	multiplex-pcr	TF	21	20	2,529,031	99.89%	16709.9
YZ400	YZ400	2021/8/8	2021/8/10	CI	Moderate	OPS	YZ	multiplex-pcr	TF	20	20	2,231,102	99.87%	14778.87
YZ401	YZ401	2021/8/2	2021/8/10	II	Moderate	OPS	YZ	multiplex-pcr	TF	30	30	357,172	99.77%	2278.9
YZ402	YZ402	2021/8/9	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	27	29	4,306,711	99.93%	15569.48
YZ403	YZ403	2021/8/6	2021/8/10	II	Moderate	OPS	YZ	multiplex-pcr	TF	25	25	1,156,317	99.77%	7172.973
YZ404	YZ404	2021/8/10	2021/8/11	CI	Moderate	OPS	YZ	multiplex-pcr	BGI	25	25	1,224,800	99.90%	4085.871
YZ405	YZ405	2021/8/9	2021/8/11	CI	Mild	OPS	YZ	multiplex-pcr	BGI	26	26	1,453,957	99.89%	4852.018
YZ406	YZ406	2021/8/7	2021/8/11	II	Moderate	OPS	YZ	multiplex-pcr	BGI	27	27	1,214,804	99.89%	4052.508

YZ407	YZ407	2021/8/4	2021/8/10	II	Mild	NPS	YZ	multiplex-pcr	TF	32	30	412,336	99.77%	2489.916
YZ408	YZ408	2021/8/10	2021/8/11	CI	Severe	NPS	YZ	multiplex-pcr	Illumina	16	18	28,494,535	99.94%	112487.6
YZ409	YZ409	2021/8/8	2021/8/10	CI	Moderate	OPS	YZ	multiplex-pcr	TF	27	25	2,508,870	99.81%	15970.54
YZ410	YZ410	2021/8/7	2021/8/10	II	Moderate	OPS	YZ	multiplex-pcr	TF	25	24	1,824,349	99.85%	12249.53
YZ411	YZ411	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	BGI	31	31	617,533	99.89%	2060.022
YZ412	YZ412	2021/8/8	2021/8/10	CI	Moderate	NPS	YZ	multiplex-pcr	TF	24	24	1,734,326	99.84%	11104.85
YZ413	YZ413	2021/8/6	2021/8/10	II	Moderate	NPS	YZ	multiplex-pcr	TF	32	30	214,632	99.77%	1359.505
YZ414	YZ414	2021/8/9	2021/8/10	CI	Mild	NPS	YZ	multiplex-pcr	TF	27	27	1,667,594	99.78%	10742.46
YZ415	YZ415	2021/8/9	2021/8/10	CI	Mild	NPS	YZ	multiplex-pcr	TF	28	28	1,153,930	99.82%	7174.557
YZ416	YZ416	2021/8/9	2021/8/10	CI	Moderate	NPS	YZ	multiplex-pcr	TF	20	22	2,983,963	99.82%	20091.1
YZ417	YZ417	2021/8/8	2021/8/10	CI	Mild	NPS	YZ	multiplex-pcr	TF	18	20	1,775,859	99.83%	11657.68
YZ418	YZ418	2021/8/8	2021/8/11	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	18	19	1,899,110	99.94%	7672.136
YZ419	YZ419	2021/8/9	2021/8/11	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	33	34	507,801	98.89%	2010.902
YZ420	YZ420	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	23	25	1,942,947	99.84%	7820.37
YZ422	YZ422	2021/8/4	2021/8/8	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	30	29	102,863	99.47%	417.3331
YZ424	YZ424	2021/8/9	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	20	21	2,281,297	99.93%	8413.484
YZ425	YZ425	2021/8/9	2021/8/10	CI	Moderate	NPS	YZ	multiplex-pcr	TF	31	32	2,101,102	99.78%	14234.28
YZ426	YZ426	2021/8/8	2021/8/10	CI	Moderate	OPS	YZ	multiplex-pcr	TF	30	29	2,229,780	99.81%	14772.75
YZ427	YZ427	2021/8/9	2021/8/10	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	35	30	3,730,192	99.88%	13639.17
YZ428	YZ428	2021/8/10	2021/8/10	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	24	24	1,656,503	99.81%	6658.233
YZ429	YZ429	2021/8/9	2021/8/10	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	35	34	3,354,830	99.94%	12838.89
YZ430	YZ430	2021/8/9	2021/8/10	CI	Mild	NPS	YZ	multiplex-pcr	TF	26	26	1,974,665	99.85%	13287.63
YZ431	YZ431	2021/8/9	2021/8/10	CI	Moderate	NPS	YZ	multiplex-pcr	TF	31	30	2,288,925	99.79%	15475.22
YZ433	YZ433	2021/8/7	2021/8/10	II	Moderate	NPS	YZ	multiplex-pcr	TF	22	24	2,458,768	99.82%	15928.28
YZ434	YZ434	2021/8/9	2021/8/10	CI	Moderate	NPS	YZ	multiplex-pcr	TF	25	25	2,354,189	99.75%	15823.29
YZ435	YZ435	2021/8/9	2021/8/10	CI	Severe	OPS	YZ	multiplex-pcr	TF	25	26	2,017,316	99.77%	13390.97
YZ436	YZ436	2021/8/7	2021/8/10	II	Mild	NPS	YZ	multiplex-pcr	Illumina	30	30	2,467,858	99.91%	9915.299
YZ438	YZ438	2021/8/4	2021/8/18	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	24	25	1,854,648	99.59%	6975.67
YZ439	YZ439	2021/8/9	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	30	30	697,645	98.89%	2372.728

YZ440	YZ440	2021/8/7	2021/8/18	II	Severe	NPS	YZ	multiplex-pcr	Illumina	23	24	9,925,468	99.94%	38033.45
YZ441	YZ441	2021/8/5	2021/8/10	II	Moderate	NPS	YZ	multiplex-pcr	TF	30	30	2,011,151	99.78%	13634.75
YZ442	YZ442	2021/8/7	2021/8/10	II	Moderate	NPS	YZ	multiplex-pcr	TF	25	26	2,190,698	99.78%	14740.3
YZ443	YZ443	2021/8/4	2021/8/10	II	Moderate	NPS	YZ	multiplex-pcr	TF	21	24	2,462,431	99.79%	16727.03
YZ444	YZ444	2021/8/9	2021/8/12	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	31	31	2,265,480	99.58%	9028.512
YZ446	YZ446	2021/8/6	2021/8/11	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	24	25	2,061,177	99.86%	8270.156
YZ448	YZ448	2021/8/10	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	25	26	25,731,971	99.87%	98132.75
YZ450	YZ450	2021/8/9	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	18	20	17,833,578	99.94%	71029.37
YZ451	YZ451	2021/8/9	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	18	20	21,514,559	99.94%	85342.05
YZ452	YZ452	2021/8/8	2021/8/10	CI	Mild	NPS	YZ	multiplex-pcr	TF	27	27	1,573,036	99.80%	10191.64
YZ453	YZ453	2021/8/5	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	24	26	19,218,774	99.79%	74832.61
YZ454	YZ454	2021/8/10	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	32	33	16,456,867	99.83%	60148.29
YZ455	YZ455	2021/8/10	2021/8/11	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	20	20	20,465,691	99.94%	81403.3
YZ456	YZ456	2021/8/10	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	28	29	641,400	99.55%	2597.14
YZ458	YZ458	2021/8/9	2021/8/11	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	18	20	1,880,124	99.94%	7588.175
YZ459	YZ459	2021/8/10	2021/8/12	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	0	33	3,311,557	99.77%	12476.32
YZ460	YZ460	2021/8/10	2021/8/11	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	29	28	802,102	99.57%	3080.047
YZ461	YZ461	2021/8/9	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	31	27	388,093	99.48%	1579.776
YZ462	YZ462	2021/8/11	2021/8/19	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	28	29	8,306,466	99.24%	28682.06
YZ463	YZ463	2021/8/11	2021/8/11	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	33	818,577	99.60%	3196.083
YZ465	YZ465	2021/8/5	2021/8/12	II	Moderate	OPS	YZ	multiplex-pcr	BGI	29	30	5,972,548	99.90%	19055.78
YZ466	YZ466	2021/8/8	2021/8/12	CI	Moderate	OPS	YZ	multiplex-pcr	BGI	24	25	14,110,668	99.94%	44831.1
YZ467	YZ467	2021/8/10	2021/8/12	CI	Mild	OPS	YZ	multiplex-pcr	BGI	24	25	11,518,392	99.94%	36399.24
YZ468	YZ468	2021/8/10	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	23	24	10,467,360	99.94%	40308.7
YZ469	YZ469	2021/8/10	2021/8/12	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	28	27	1,136,282	99.60%	4600.826
YZ470	YZ470	2021/8/10	2021/8/12	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	31	30	1,097,410	99.58%	4439.936
YZ471	YZ471	2021/8/10	2021/8/12	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	29	28	1,287,959	99.45%	5133.955
YZ472	YZ472	2021/8/10	2021/8/11	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	31	32	2,297,388	99.78%	9165.181
YZ473	YZ473	2021/8/10	2021/8/12	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	36	35	1,794,043	99.86%	7218.252

YZ475	YZ475	2021/8/10	2021/8/11	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	30	30	762,025	99.57%	2980.38
YZ478	YZ478	2021/8/7	2021/8/11	II	Moderate	NPS	YZ	multiplex-pcr	Illumina	22	22	24,686,913	99.94%	95555.85
YZ480	YZ480	2021/8/10	2021/8/12	CI	Moderate	OPS	YZ	multiplex-pcr	BGI	22	24	13,775,207	99.94%	43777.45
YZ481	YZ481	2021/8/10	2021/8/12	CI	Severe	OPS	YZ	multiplex-pcr	BGI	30	30	184,753	99.72%	593.9336
YZ484	YZ484	2021/8/11	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	31	6,065,307	99.72%	23073.52
YZ485	YZ485	2021/8/10	2021/8/12	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	33	34	26,732,537	99.93%	105802.9
YZ486	YZ486	2021/8/10	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	25	25	6,361,492	99.89%	24114.53
YZ488	YZ488	2021/8/10	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	23	24	11,791,744	99.94%	44919.96
YZ489	YZ489	2021/8/11	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	25	25	6,090,301	99.94%	23121.42
YZ492	YZ492	2021/8/10	2021/8/12	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	30	2,829,372	99.63%	11461.95
YZ494	YZ494	2021/8/9	2021/8/12	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	19	20	1,579,525	99.61%	6290.944
YZ497	YZ497	2021/8/11	2021/8/12	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	20	21	1,100,006	99.60%	4457.015
YZ498	YZ498	2021/8/6	2021/8/18	II	Mild	OPS	YZ	multiplex-pcr	Illumina	28	29	10,672,340	99.93%	41085.47
YZ499	YZ499	2021/8/12	2021/8/13	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	26	27	1,679,771	99.86%	6713.408
YZ500	YZ500	2021/8/11	2021/8/18	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	24	25	10,123,903	99.91%	38797.16
YZ504	YZ504	2021/8/10	2021/8/18	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	29	29	1,131,290	99.45%	3987.386
YZ505	YZ505	2021/8/12	2021/8/18	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	25	26	399,825	98.99%	1495.327
YZ506	YZ506	2021/8/11	2021/8/13	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	25	32	358,592	99.02%	1394.056
YZ507	YZ507	2021/8/11	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	32	33	4,194,722	99.93%	16049.52
YZ509	YZ509	2021/8/10	2021/8/18	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	32	33	2,897,692	99.86%	10708
YZ510	YZ510	2021/8/10	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	27	27	8,878,686	99.94%	33662.13
YZ512	YZ512	2021/8/11	2021/8/13	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	23	27	1,423,963	99.88%	5715.885
YZ514	YZ514	2021/8/12	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	25	25	2,730,071	99.64%	10381.09
YZ515	YZ515	2021/8/12	2021/8/16	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	31	34	701,680	99.75%	2625.356
YZ516	YZ516	2021/8/9	2021/8/16	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	25	26	1,578,775	99.83%	6312.204
YZ517	YZ517	2021/8/12	2021/8/16	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	30	28	1,689,086	99.84%	6751.423
YZ518	YZ518	2021/8/12	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	18	19	10,403,785	99.93%	36565.65
YZ519	YZ519	2021/8/12	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	23	24	1,383,281	99.88%	4847.055
YZ522	YZ522	2021/8/12	2021/8/13	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	23	24	980,260	99.76%	3782.601

YZ523	YZ523	2021/8/12	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	28	29	889,943	99.59%	3267.013
YZ524	YZ524	2021/8/13	2021/8/14	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	24	25	1,437,113	99.90%	5781.894
YZ525	YZ525	2021/8/12	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	19	20	11,534,996	99.91%	44240.5
YZ526	YZ526	2021/8/10	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	29	30	15,000,466	99.94%	55482.26
YZ531	YZ531	2021/8/13	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	17	18	10,735,438	99.94%	40623.74
YZ532	YZ532	2021/8/13	2021/8/15	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	16	18	1,704,304	99.55%	6373.416
YZ534	YZ534	2021/8/13	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	22	23	4,891,887	99.93%	18559.2
YZ535	YZ535	2021/8/13	2021/8/15	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	31	27	508,379	99.58%	2033.586
YZ536	YZ536	2021/8/14	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	19	20	26,301,042	99.94%	99605.61
YZ537	YZ537	2021/8/13	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	21	22	11,139,714	99.94%	42842.83
YZ539	YZ539	2021/8/11	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	27	27	13,756,097	99.92%	51334.64
YZ540	YZ540	2021/8/4	2021/8/14	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	23	24	790,282	99.82%	3174.38
YZ541	YZ541	2021/8/13	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	30	8,803,186	99.94%	33754.01
YZ542	YZ542	2021/8/13	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	19	20	6,817,804	99.91%	25319.28
YZ545	YZ545	2021/8/13	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	26	27	12,309,648	99.94%	47530.96
YZ546	YZ546	2021/8/13	2021/8/15	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	30	30	165,921	99.70%	668.936
YZ547	YZ547	2021/8/14	2021/8/18	CI	Mild	OPS	YZ	multiplex-pcr	Illumina	31	32	11,897,197	99.94%	45605.08
YZ548	YZ548	2021/8/13	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	18	19	11,881,278	99.94%	45815.42
YZ549	YZ549	2021/8/10	2021/8/15	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	33	31	385,667	99.41%	1536.305
YZ551	YZ551	2021/8/15	2021/8/19	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	29	30	12,026,776	99.91%	45284.34
YZ552	YZ552	2021/8/15	2021/8/18	CI	Mild	NPS	YZ	multiplex-pcr	Illumina	22	23	1,599,325	99.63%	5909.415
YZ553	YZ553	2021/8/15	2021/8/18	CI	Moderate	NPS	YZ	multiplex-pcr	Illumina	27	28	12,219,751	99.94%	46040.41
YZ554	YZ554	2021/8/5	2021/8/17	II	Moderate	OPS	YZ	multiplex-pcr	Illumina	29	30	1,866,221	99.92%	7289.246
YZ559	YZ559	2021/8/16	2021/8/17	ER	Moderate	OPS	YZ	multiplex-pcr	Illumina	22	24	2,026,302	99.92%	7550.223
YZ560	YZ560	2021/8/16	2021/8/16	ER	Mild	OPS	YZ	multiplex-pcr	Illumina	33	33	779,946	99.89%	2702.612
YZ561	YZ561	2021/8/16	2021/8/18	ER	Mild	OPS	YZ	multiplex-pcr	Illumina	32	33	6,410,587	99.85%	25273.11
YZ562	YZ562	2021/8/10	2021/8/18	CI	Moderate	OPS	YZ	multiplex-pcr	Illumina	29	30	6,127,909	99.85%	24298.09
YZ564	YZ564	2021/8/16	2021/8/18	ER	Moderate	OPS	YZ	multiplex-pcr	Illumina	29	31	5,532,590	99.90%	21918.26
YZ570	YZ570	2021/8/25	2021/8/18	ER	Mild	OPS	YZ	multiplex-pcr	Illumina	28	29	6,392,719	99.71%	22901.38

NJ/Yu	NJ/Yu	2021/7/10	2021/7/10	NA	Asympt	OPS	NJ	multiplex-pcr	Illumina
	XB		2021/5/14				Jiangsu import		
	XSG		2021/6/13				Jiangsu import		
	GSF		2021/6/17				Jiangsu import		
	ZYC		2021/6/22				Jiangsu import		
	CXJ		2021/6/22				Jiangsu import		
	BN		2021/6/22				Jiangsu import		
	IVDC-06-01		2021/6/6				GD		
	IVDC-0610-39		2021/6/25				GD		
	IVDC-0610-01		2021/6/11				GD		
	IVDC-05-01		2021/4/17				GD		
	Ruili-IVDC-04-01		2021/3/31				YN		
	Ruili-IVDC-04-02		2021/3/30				YN		
	YN-01		2021/6/17				YN		
	YN-47		2021/7/8				YN		
	DL-ILBS-22053		2020/6/13				New Delhi		

OPS= Oropharyngeal swab. NPS= Nasopharyngeal Swab. NJ=Nanjing. YZ=Yangzhou. GD=Guangdong. YN=Yunnan. TF= Thermo Fisher.